

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52, Search time 38.9691 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-1

Perfect score: 24

Sequence: 1 agtcgtacggagatcgagataaat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/5C_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/5D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	24	100.0	945 3	US-08-816-977-1
2	24	100.0	945 4	US-09-334-477-1
3	24	100.0	969 3	US-08-816-977-20
4	24	100.0	969 4	US-09-334-477-20
5	24	100.0	981 3	US-08-816-977-36
6	24	100.0	981 4	US-09-334-477-36
7	24	100.0	1241 3	US-08-816-977-9
8	24	100.0	1241 4	US-09-334-477-9
9	24	100.0	2073 3	US-08-816-977-46
10	24	100.0	2073 4	US-09-334-477-46
11	24	100.0	2127 3	US-08-816-977-32
12	24	100.0	2127 4	US-09-334-477-32
13	24	100.0	48908 3	US-09-453-702B-137
14	17.6	73.3	774 4	US-09-583-110-1639
15	17.2	71.7	150 4	US-08-979-847B-36
16	17.2	71.7	297 1	US-08-471-724-2
17	17.2	71.7	297 2	US-08-471-969-2
18	17.2	71.7	297 3	US-08-384-137-2
19	17.2	71.7	297 4	US-08-470-006A-2
20	17.2	71.7	297 5	US-08-691-563C-2
21	17.2	71.7	297 6	US-09-200-990-2
22	17.2	71.7	297 7	US-09-133-411-2
23	17.2	71.7	297 8	US-09-374-766-2
24	17.2	71.7	299 3	US-08-979-847B-2
25	17.2	71.7	299 4	US-08-691-563C-40
26	17.2	71.7	299 5	US-09-374-766-40
27	17.2	71.7	1158 1	US-08-471-724-1

28	17.2	71.7	1158 2	US-08-471-969-1
29	17.2	71.7	1158 3	US-08-384-137-1
30	17.2	71.7	1158 4	US-08-470-006A-1
31	17.2	71.7	1158 5	US-08-691-563C-1
32	17.2	71.7	1158 6	US-09-200-990-1
33	17.2	71.7	1158 7	US-09-133-411-1
34	17.2	71.7	1158 8	US-09-374-766-1
35	17.2	71.7	1158 9	US-08-979-847B-1
36	17.2	71.7	1597 4	US-08-979-847B-205
37	17.2	71.7	1600 4	US-08-979-847B-206
38	17.2	71.7	1600 5	US-08-979-847B-207
39	17.2	71.7	2304 4	US-08-979-847B-87
40	17.2	71.7	2364 4	US-08-979-847B-88
41	17.2	71.7	2391 4	US-08-691-563C-57
42	17.2	71.7	2391 5	US-09-374-766-57
43	17.2	71.7	2391 6	US-08-979-847B-53
44	16.6	69.2	1230025 4	US-09-128-452A-1
45	16	66.7	256 4	US-09-313-294A-938

ALIGNMENTS

RESULT 1
US-08-816-977-1

Sequence 1, Application US/08816977

Patent No. 6080400

GENERAL INFORMATION:

APPLICANT: Williams, James A.

APPLICANT: Byrne, Lisa M.

APPLICANT: Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of

TITLE OF INVENTION: Vertotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESSES:

ADDRESSER: Medien & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/816,977

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPMD-02450

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 945 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..945

US-08-816-977-1

Query Match

Best Local Similarity 100.0%; Score 24; DB 3; Length 945;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 : Search time 195.093 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-1
Perfect score: 24
Sequence: 1 agtcgtacggggatgcagataat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	39	US-10-085-056-28
2	24	100.0	502	US-10-425-821-93
3	24	100.0	879	US-10-765-580-9
4	24	100.0	945	US-09-334-477-1
5	24	100.0	969	US-09-334-477-20
6	24	100.0	981	US-09-334-477-36
7	24	100.0	1241	US-09-334-477-9
8	24	100.0	1507	US-10-765-580-11
9	24	100.0	2073	US-09-334-477-46
10	24	100.0	2127	US-09-334-477-32
11	24	100.0	48908	US-10-114-170-137
12	17.6	73.3	581	US-10-027-632-221193

13	17.6	73.3	581	15	US-10-027-632-221193	Sequence 221193, A
14	17.6	73.3	1414	15	US-10-369-493-36750	Sequence 36750, A
15	17.2	71.7	150	8	US-08-979-847-36	Sequence 36, Appl
16	17.2	71.7	150	15	US-10-114-104-36	Sequence 36, Appl
17	17.2	71.7	297	8	US-08-979-847-2	Sequence 2, Appl
18	17.2	71.7	297	15	US-10-430-442-2	Sequence 2, Appl
19	17.2	71.7	297	15	US-10-114-104-2	Sequence 2, Appl
20	17.2	71.7	299	15	US-10-430-442-40	Sequence 40, Appl
21	17.2	71.7	1158	8	US-08-979-847-1	Sequence 1, Appl
22	17.2	71.7	1158	15	US-10-430-442-1	Sequence 1, Appl
23	17.2	71.7	1158	15	US-10-114-104-1	Sequence 1, Appl
24	17.2	71.7	1597	15	US-08-979-847-205	Sequence 205, App
25	17.2	71.7	1597	15	US-10-114-104-205	Sequence 205, App
26	17.2	71.7	1600	8	US-08-979-847-206	Sequence 206, App
27	17.2	71.7	1600	8	US-08-979-847-207	Sequence 207, App
28	17.2	71.7	1600	15	US-10-114-104-206	Sequence 207, App
29	17.2	71.7	1600	15	US-10-114-104-207	Sequence 87, Appl
30	17.2	71.7	2304	8	US-08-979-847-87	Sequence 87, Appl
31	17.2	71.7	2304	15	US-10-114-104-87	Sequence 88, Appl
32	17.2	71.7	2365	8	US-08-979-847-88	Sequence 88, Appl
33	17.2	71.7	2365	15	US-10-114-104-88	Sequence 53, Appl
34	17.2	71.7	2391	8	US-08-979-847-53	Sequence 53, Appl
35	17.2	71.7	2391	15	US-10-430-442-57	Sequence 87, Appl
36	17.2	71.7	2391	15	US-10-114-104-53	Sequence 88, Appl
37	16.8	70.0	1688	16	US-10-425-114-36262	Sequence 36262, A
38	16.8	70.0	2802	18	US-10-425-114-36499	Sequence 36499, A
39	16.8	70.0	3068	17	US-10-437-963-3598	Sequence 3598, Ap
40	16.8	70.0	3068	18	US-10-437-963-3598	Sequence 165722, A
41	16.6	69.2	456	13	US-10-027-632-40457	Sequence 40457, A
42	16.6	69.2	456	15	US-10-027-632-40457	Sequence 1040, Ap
43	16.6	69.2	525	9	US-09-728-444-1040	Sequence 35369, A
44	16.6	69.2	556	13	US-10-027-632-35369	
45	16.6	69.2	556	13	US-10-027-632-35369	

ALIGNMENTS

RESULT 1
US-10-085-056-28/c
Sequence 28, Application US/10085056
Publication No. US20030008305A1
GENERAL INFORMATION:
APPLICANT: MARUYAMA, TAKAHIRO
APPLICANT: ISHIGURO, TAKAHIRO
TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
FILE REFERENCE: 220081US0
CURRENT FILING DATE: 2002-05-30
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-10-085-056-28

Query Match 100.0%; Score 24; DB 14; length 39;
Best local similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCGTACGGGGATGAGTAAT 24
DB 29 AGTCGTACGGGGATGAGTAAT 6

RESULT 2
US-10-425-821-93

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 184.701 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-1

Perfect score: 1 agcgtacggggatgcagataaat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	5	AA61478 EHEC huma
2	24	100.0	39	6	ABN84751 Oligonuc
3	24	100.0	287	12	ADN02037 Enteroha
4	24	100.0	870	10	ADL14887 DNA enco
5	24	100.0	945	2	AA742649 Verotoxin
6	24	100.0	945	3	AA551194 E. coli v
7	24	100.0	945	6	ABK11775 E. coli v
8	24	100.0	948	4	AAH01085 Escherich
9	24	100.0	969	4	AA742663 Histidine
10	24	100.0	969	6	AA551208 Recombina
11	24	100.0	969	6	ABK11789 CDNA enco
12	24	100.0	980	2	AA742673 FLAG tag/
13	24	100.0	981	3	AA551218 FLAG tag-
14	24	100.0	981	6	ABK11799 CDNA enco
15	24	100.0	1192	2	AAV11402 Shiga tox
16	24	100.0	1207	2	AAV11403 Shiga tox
17	24	100.0	1227	11	ADL25576 S. dysent
18	24	100.0	1227	11	ADL25577 S. sonnei
19	24	100.0	1227	11	ADL25575 Bacteriop
20	24	100.0	1230	2	AAQ12711 Shiga-11k
21	24	100.0	1230	2	AA791637 Phage H19

22	24	100.0	1230	2	AA230662 E.coli ba
23	24	100.0	1230	3	AA290018 E. coli b
24	24	100.0	1235	2	AAV11404 Shiga tox
25	24	100.0	1241	2	AA742653 Sequence
26	24	100.0	1241	3	AA551198 DNA direc
27	24	100.0	1241	6	ABK11779 Polycistr
28	24	100.0	1369	2	AA227687 Verotoxin
29	24	100.0	1389	2	AAV11400 Shiga tox
30	24	100.0	2073	3	AA551226 MBP-VT-1
31	24	100.0	2073	6	ABK11957 CDNA enco
32	24	100.0	2126	2	AA742671 Maltose b
33	24	100.0	2127	3	AA551216 MBP-VT-1
34	24	100.0	2127	6	ABK11797 CDNA enco
35	24	100.0	47879	10	ADCC0509 Enteroha
36	24	100.0	48908	9	ACD19124 E. coli 0
37	23	95.8	35	8	ABX94713 EHEC SLT1
38	17.2	71.7	150	2	AA796481 Fragment
39	17.2	71.7	150	2	AAV43153 Multiple
40	17.2	71.7	150	9	ADB84331 MSRV-1 PO
41	17.2	71.7	150	12	ADG14777 MSRV-1 PO
42	17.2	71.7	297	2	AA702816 Multiple
43	17.2	71.7	297	2	AA737974 MSRV-1 PO
44	17.2	71.7	297	2	AA796526 MSRV-1B c
45	17.2	71.7	297	2	AAV43116 Multiple

ALIGNMENTS

RESULT 1	AA61478 standard; DNA; 24 BP.
ID	AA61478
XX	AA61478;
AC	18-JUN-2001 (first entry)
XX	
DT	
XX	EHEC human pathogen strx1 PCR primer SEQ ID 1.
DE	
XX	EHEC infection; multiplex amplification; detection; human; pig;
KW	enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; ss.
XX	
OS	Escherichia coli.
XX	
PN	DE19946296-A1.
PD	29-MAR-2001.
XX	
PF	28-SEP-1999; 99DE-01046296.
XX	
PR	28-SEP-1999; 99DE-01046296.
XX	
PA	(HOPE) ROCHE DIAGNOSTICS GMBH.
XX	
PI	Gunzer F, Bellin T;
XX	
DR	WPI; 2001-246145/26.
XX	
PT	Primers for amplifying Shiga toxin sequences in Escherichia coli; useful
PT	in multiplex amplification detection of enterohemorrhagic strains.
XX	
PS	Claim 1; Page 10; 14p; German.
XX	
CC	This invention describes a novel primer (PI) which can be used in a
CC	multiplex amplification reaction for detecting clinically important EHEC
CC	(enterohemorrhagic Escherichia coli) infections. PI allow simultaneous
CC	detection of human and pig pathogens in a single measurement
XX	
SQ	Sequence 24 BP; 8 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match	100.0%; Score 24; DB 5; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.035;
Matches	24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 184.701 Seconds
(without alignments)
682,108 Million cell updates/sec

Title: US-10-089-487-2

Sequence: 1 ccgaccacataagaagaactcat 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23sep04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	AAF61479	AAf61479 EHEC huma
2	24	100.0	945	AAT42649	Aat42649 Verotoxin
3	24	100.0	945	AAAS1194	AAas1194 E. coli v
4	24	100.0	945	ABK11775	ABk11775 E. coli v
5	24	100.0	969	AAT42663	Aat42663 Histidine
6	24	100.0	969	AAAS1208	AAas1208 Recombina
7	24	100.0	969	ABK11789	ABk11789 CDNA enco
8	24	100.0	980	AAT42673	Aat42673 Flag tag/
9	24	100.0	981	AAAS1218	AAas1218 FLAG tag-
10	24	100.0	981	ABK11799	ABk11799 CDNA enco
11	24	100.0	1192	AAV11402	AAv11402 Shiga tox
12	24	100.0	1207	AAV11403	AAv11403 Shiga tox
13	24	100.0	1227	AD125576	Ad125576 S. dysent
14	24	100.0	1227	AD125577	Ad125577 S. sonnei
15	24	100.0	1227	AD125578	Ad125578 Bacterioph
16	24	100.0	1230	AAQ12711	AAq12711 Shiga-lik
17	24	100.0	1230	AAT91637	Aat91637 Phage H19
18	24	100.0	1230	AAZ30662	AAz30662 E. coli ba
19	24	100.0	1230	AAZ99018	AAz99018 E. coli b
20	24	100.0	1235	AAV11404	AAv11404 Shiga tox
21	24	100.0	1241	AA742653	AA742653 Sequence

C 22	24	100.0	1241	3	AAAS1198	AAas1198 DNA direc
C 23	24	100.0	1369	2	AAZ27687	Aaz27687 Verotoxin
C 24	24	100.0	1389	2	AAV11400	AAv11400 Shiga tox
C 25	24	100.0	2073	3	AAAS1226	AAas1226 MBP-VT-1
C 26	24	100.0	2073	6	ABK11957	ABk11957 CDNA enco
C 27	24	100.0	2126	2	AAT42671	Aat42671 Maltose b
C 28	24	100.0	2127	3	AAAS1216	AAas1216 MBP-VT-1
C 29	24	100.0	2127	6	ABK11797	ABk11797 CDNA enco
C 30	24	100.0	47879	10	ADC00509	Adc00509 Enterohae
C 31	24	100.0	48908	9	ACD19124	Ac19124 E. coli 0
C 32	23.6	98.3	33	6	ABO87914	ABo87914 Enterohae
C 33	22.4	93.3	948	4	AAH01085	AAh01085 Escherich
C 34	22.4	93.3	1241	6	ABK11779	ABk11779 Polyclon
C 35	19	79.2	1072	2	AAT86332	Aat86332 BPI pepti
C 36	17.8	74.2	2155	10	ADB52356	Adb52356 Primary r
C 37	17.8	74.2	2155	10	ADL16217	Adl16217 Rat prote
C 38	17.8	74.2	134525	2	AAO04525	Aao04525 Total bas
C 39	17.6	73.3	3633	8	ABT18908	ABt18908 Aspergill
C 40	17.6	73.3	3741	8	ABT20130	ABt20130 Aspergill
C 41	17.6	73.3	3741	8	ABT20728	ABt20728 Aspergill
C 42	17.6	73.3	3741	8	ABT18314	ABt18314 Aspergill
C 43	17.6	73.3	5741	8	ABT19534	ABt19534 Aspergill
C 44	17.6	73.3	5741	8	ABT17720	ABt17720 Aspergill
C 45	17.6	73.3	300000	10	ADB6352	Adb6352 Human PTP

ALIGNMENTS

RESULT 1
ID AAF61479 standard; DNA; 24 BP.
XX AAF61479;
AC AAF61479;
XX 18-JUN-2001 (first entry)
XX DE EHEC human pathogen sexual PCR primer SEQ ID 2.
XX DE EHEC infection; multiplex amplification; detection; human; pig;
XX KW enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; ss.
XX OS Escherichia coli.
XX EN DE19946296-A1.
XX PD 29-MAR-2001.
XX PF 28-SEP-1999; 99DE-01046296.
XX PF 28-SEP-1999; 99DE-01046296.
XX PR 28-SEP-1999; 99DE-01046296.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PI Gunzer F, Bellin T;
XX PT WPI, 2001-246145/26.
XX PT Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
XX PT in multiplex amplification detection of enterohemorrhagic strains.
XX PS Claim 1; Page 10; 14pp; German.
XX CC This invention describes a novel primer (P1) which can be used in a
XX CC multiplex amplification reaction for detecting clinically important EHEC
XX CC (enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous
XX CC detection of human and pig pathogens in a single measurement
SQ Sequence 24 BP; 10 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 195.093 seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-2

Perfect score: 24
Sequence: 1 ccggacacatagaagaactcat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	100.0	879 17	US-10-765-580-9 Sequence 9, Appl
C 3	24	100.0	945 9	US-09-334-477-1 Sequence 1, Appl
C 4	24	100.0	969 9	US-09-334-477-20 Sequence 20, Appl
C 5	24	100.0	981 9	US-09-334-477-36 Sequence 36, Appl
C 6	24	100.0	1241 9	US-09-334-477-9 Sequence 9, Appl
C 7	24	100.0	1507 17	US-10-765-580-11 Sequence 11, Appl
C 8	24	100.0	2073 9	US-09-334-477-46 Sequence 46, Appl
C 9	24	100.0	2127 9	US-09-334-477-32 Sequence 32, Appl
C 10	24	100.0	48908 14	US-10-114-170-137 Sequence 137, Appl
C 11	23.6	98.3	33 17	US-10-250-997-13 Sequence 13, Appl
C 12	19	79.2	70 15	US-10-127-890-73 Sequence 73, Appl

13	19	79.2	78	15	US-10-127-890-74
C 14	19	75.8	1072	9	US-09-765-527-250
15	18.2	75.8	142947	18	US-10-719-993-6967
16	17.8	74.2	201	18	US-10-719-993-26595
C 17	17.8	74.2	2155	15	US-10-437-963-47556
18	17.8	74.2	2155	15	US-10-366-547-66
C 19	17.8	74.2	33271	18	US-10-719-993-6996
20	17.8	74.2	786452	18	US-10-719-993-6996
21	17.6	73.3	1280	13	US-10-027-632-124418
22	17.6	73.3	1280	15	US-10-027-632-124418
23	17.6	73.3	3633	15	US-10-128-714-2078
24	17.6	73.3	3741	15	US-10-128-714-1078
25	17.6	73.3	3741	15	US-10-128-714-6078
26	17.6	73.3	3741	15	US-10-128-714-7078
27	17.6	73.3	5741	15	US-10-128-714-78
28	17.6	73.3	5741	15	US-10-128-714-5078
C 29	17.6	73.3	107745	17	US-10-398-221-10
C 30	17.6	73.3	300000	15	US-10-398-221-2058
C 31	17.6	73.3	300000	15	US-10-398-221-2058
C 32	17.4	72.5	1249	13	US-10-027-632-123375
C 33	17.4	72.5	1249	15	US-10-027-632-123375
C 34	17.4	72.5	1163020	16	US-10-398-221-10
C 35	17.4	72.5	3011208	16	US-10-398-221-2058
36	17.2	71.7	230	15	US-10-106-698-2194
C 37	17.2	71.7	370	18	US-10-425-115-55577
38	17.2	71.7	620	17	US-10-437-963-39794
C 39	17.2	71.7	758	15	US-10-012-697-1050
40	17.2	71.7	2484	15	US-10-325-881-68
C 41	17.2	71.7	2679	15	US-10-369-493-40501
42	17.2	71.7	2859	15	US-10-094-749-1325
C 43	17.2	71.7	7734	9	US-09-764-868-1317
44	17.2	71.7	21184	15	US-10-017-161-703
45	17.2	71.7	48459	13	US-10-087-192-424

ALIGNMENTS

RESULT 1
US-10-425-821-91/c
; Sequence 91, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos,e
; APPLICANT: BERKAL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-425-821-91

Query Match 100.0%; Score 24; DB 18; Length 583;
Best Local Similarity 100.0%; Pred. NO. 0.27; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0

QY 1 CCGACACATAGAGAACTCAT 24
DB 247 CCGACACATAGAGAACTCAT 224

RESULT 2
US-10-765-580-9/c
; Sequence 9, Application US/10765580
; Publication No. US20040165565A1
; GENERAL INFORMATION:
; APPLICANT: Backer, Marina V.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 32.4742 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-3

Perfect score: 20
Sequence: 1 ttccggaatgcaatcagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	20	100.0	954	4	US-09-334-477-5
4	20	100.0	981	3	US-08-816-977-24
5	20	100.0	981	4	US-09-334-477-24
6	20	100.0	990	3	US-08-816-977-38
7	20	100.0	990	4	US-09-334-477-38
8	20	100.0	1235	3	US-08-816-977-10
9	20	100.0	1235	4	US-09-334-477-10
10	20	100.0	1235	4	US-09-599-032A-3
11	20	100.0	2085	3	US-08-816-977-48
12	20	100.0	2085	4	US-09-334-477-48
13	20	100.0	2136	3	US-08-816-977-34
14	20	100.0	2136	4	US-09-334-477-34
15	20	100.0	61663	3	US-09-453-7028-62
16	15.8	79.0	1664976	4	US-08-916-421B-1
17	15.8	79.0	1664976	4	US-09-692-570-1
18	15.4	77.0	240	4	US-09-489-039A-1762
19	15.4	77.0	636	4	US-09-270-767-2119
20	15.4	77.0	636	4	US-09-270-767-17401
21	15.2	76.0	252	3	US-08-905-223-245
22	15.2	76.0	2039	4	US-08-849-602-12
23	15.2	76.0	2273	2	US-08-788-539A-1
24	15.2	76.0	3343	3	US-08-965-762-19
25	15.2	76.0	3343	4	US-09-911-927-19
26	15.2	76.0	3343	4	US-09-911-927-21
27	15.2	76.0	3343	4	US-09-911-882-19

28	15.2	76.0	3343	4	US-09-911-882-21	Sequence 21, Appl
29	15.2	76.0	3343	4	US-09-911-888-19	Sequence 19, Appl
30	15.2	76.0	3343	4	US-09-911-888-21	Sequence 21, Appl
31	15.2	76.0	4164	1	US-08-188-582-3	Sequence 3, Appl
32	15.2	76.0	4164	1	US-08-646-715-3	Sequence 3, Appl
33	15.2	76.0	18431	4	US-09-221-017B-1090	Sequence 1090, Ap
34	15.2	76.0	41	3	US-09-289-751-3	Sequence 3, Appl
35	14.8	74.0	385	4	US-09-513-995C-34730	Sequence 34730, A
36	14.8	74.0	1098	4	US-09-270-767-11546	Sequence 11546, A
37	14.8	74.0	1272	4	US-09-248-796A-2376	Sequence 2376, Ap
38	14.8	74.0	1386	4	US-09-248-796A-2376	Sequence 13, Appl
39	14.8	74.0	4953	4	US-09-602-787A-55	Sequence 55, Appl
40	14.8	74.0	4953	4	US-09-602-787A-55	Sequence 3, Appl
41	14.8	74.0	99916	4	US-09-816-095-3	Sequence 3, Appl
42	14.4	72.0	32	4	US-09-828-303-34	Sequence 34, Appl
43	14.4	72.0	354	4	US-09-513-995C-34934	Sequence 34934, A
44	14.4	72.0	3001	4	US-09-539-333D-214	Sequence 214, App
45	14.4	72.0	41100	4	US-09-755-665-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-147-251-1
Sequence 1, Application US/09147251
Patent No. 6391546
GENERAL INFORMATION:
APPLICANT: KARUBE, Isao
APPLICANT: SAMURA, Shinya
APPLICANT: NAGATA, Ryohel
TITLE OF INVENTION: METHOD FOR DETECTING TARGET NUCLEOTIDE SEQUENCE
FILE REFERENCE: 7867-0002-0XPCT
CURRENT APPLICATION NUMBER: US/09/147,251
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: JP117735/1997
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: JP74442/1998
EARLIER FILING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP123371/1998
EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 540
TYPE: DNA
ORGANISM: Escherichia coli
US-09-147-251-1

Query Match 100.0%; Score 20; DB 3; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGATGCAATCAGTC 20
DB 441 TTCCGGATGCAATCAGTC 460

RESULT 2
US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
NUMBER OF SEQUENCES: 49
TITLE OF INVENTION: Verotoxin-Induced Disease
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 162.577 Seconds
(without alignments) 706.850 Million cell updates/sec

Title: US-10-089-487-3
Perfect score: 20
Sequence: 1 ttccggaatgcattcagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	540	14	US-10-103-798-1
3	20	100.0	540	15	US-10-334-831-1
4	20	100.0	954	9	US-09-334-477-5
5	20	100.0	981	9	US-09-334-477-24
6	20	100.0	990	9	US-09-334-477-38
7	20	100.0	1235	9	US-09-334-477-10
8	20	100.0	1612	9	US-09-870-759-27
9	20	100.0	1612	10	US-09-751-708A-27
10	20	100.0	1612	18	US-10-428-817A-23
11	20	100.0	1612	18	US-10-425-821-92
12	20	100.0	2085	9	US-09-334-477-48

13	20	100.0	2136	9	US-09-334-477-34	Sequence 34, Appl
14	20	100.0	61662	16	US-10-418-837-1	Sequence 1, Appl
15	20	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl
16	16.8	84.0	4689	16	US-10-282-122A-33564	Sequence 33564, A
17	16.8	84.0	5855	18	US-10-783-528-52	Sequence 52, Appl
18	16.8	84.0	38234	13	US-10-087-192-1762	Sequence 1762, Ap
19	16.4	82.0	810	15	US-10-369-497-32514	Sequence 32514, A
20	15.8	79.0	704	18	US-10-653-047-5739	Sequence 5739, Ap
21	15.8	79.0	1080	15	US-10-369-493-41357	Sequence 41357, A
22	15.8	79.0	1536	18	US-10-425-115-25113	Sequence 25113, A
23	15.8	79.0	1549	17	US-10-767-701-13781	Sequence 13781, A
24	15.8	79.0	2303	18	US-10-425-115-23429	Sequence 23429, A
25	15.8	79.0	173808	13	US-10-003-806-10	Sequence 10, Appl
26	15.4	77.0	201	16	US-10-282-122A-19911	Sequence 19911, A
27	15.4	77.0	201	16	US-10-282-122A-23805	Sequence 23805, A
28	15.4	77.0	3614	17	US-10-767-701-27245	Sequence 27245, A
29	15.4	77.0	494	13	US-10-027-633-311865	Sequence 311865, A
30	15.4	77.0	494	15	US-10-027-633-311865	Sequence 311865, A
31	15.4	77.0	497	13	US-10-027-633-57834	Sequence 57834, A
32	15.4	77.0	497	13	US-10-027-633-57834	Sequence 57834, A
33	15.4	77.0	612	13	US-10-027-633-5921	Sequence 5921, Ap
34	15.4	77.0	612	15	US-10-027-633-5921	Sequence 5921, Ap
35	15.4	77.0	3063	16	US-10-424-599-39847	Sequence 39847, A
36	15.4	77.0	3575	16	US-10-424-599-106545	Sequence 106545, A
37	15.2	76.0	180	14	US-10-198-846-10248	Sequence 10248, A
38	15.2	76.0	359	9	US-09-864-761-24185	Sequence 24185, A
39	15.2	76.0	375	18	US-10-425-115-39740	Sequence 39740, A
40	15.2	76.0	473	10	US-09-918-995-2619	Sequence 2619, Ap
41	15.2	76.0	476	14	US-10-198-846-63	Sequence 63, Appl
42	15.2	76.0	558	9	US-09-864-761-7471	Sequence 7471, Appl
43	15.2	76.0	558	17	US-10-767-701-16023	Sequence 16023, A
44	15.2	76.0	562	16	US-10-259-194A-526	Sequence 526, App
45	15.2	76.0	567	18	US-10-357-930-60418	Sequence 60418, A

ALIGNMENTS

RESULT 1
US-10-425-821-94
Sequence 94, Application US/10425821
Publication NO. US20040219530A1
GENERAL INFORMATION:
APPLICANT: BROUSSEAU, Roland
APPLICANT: HAREL, Jos'e
APPLICANT: BEKAL, Sadi'a
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCES: 86369-3
CURRENT APPLICATION NUMBER: US/10/425, 821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn version 3.2
SEQ ID NO 94
LENGTH: 482
TYPE: DNA
ORGANISM: Escherichia coli
US-10-425-821-94

Query Match 100.0%; Score 20; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGAATGCATTGATC 20
DB 294 TTCCGGAATGCATTGATC 313

RESULT 2
US-10-103-798-1
Sequence 1, Application US/10103798
Publication NO. US20030054378A1
GENERAL INFORMATION:
APPLICANT: KARUBE, Isao

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 161.613 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21
Sequence: 1 cgatactccggaagacatcg 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	5	AAF61481
2	21	100.0	954	2	AAT42651
3	21	100.0	954	3	AAAS1196
4	21	100.0	954	6	ABK11777
5	21	100.0	960	10	ADH34345
6	21	100.0	960	10	ADH34301
7	21	100.0	960	10	ADH34339
8	21	100.0	960	10	ADH34337
9	21	100.0	960	10	ADH34339
10	21	100.0	960	10	ADH34337
11	21	100.0	960	10	ADH34335
12	21	100.0	980	2	AAT42665
13	21	100.0	981	6	ABK11791
14	21	100.0	989	2	AAT42674
15	21	100.0	990	3	AAAS1219
16	21	100.0	990	6	ABK11800
17	21	100.0	1201	2	AAV11405
18	21	100.0	1217	2	AAV11406
19	21	100.0	1232	11	ADL25585
20	21	100.0	1232	11	ADL25580
21	21	100.0	1232	11	ADL25580 E. coli s

C 22	21	100.0	1232	11	ADL25578	AdL25578 E. coli s
C 23	21	100.0	1235	2	AAT42654	Aat42654 Sequence
C 24	21	100.0	1235	3	AAAS1199	AAAS1199 DNA direc
C 25	21	100.0	1235	6	ABK11780	ABK11780 Polyclastr
C 26	21	100.0	1235	11	ADL25584	AdL25584 E. coli s
C 27	21	100.0	1235	11	ADL25583	AdL25583 E. coli s
C 28	21	100.0	1242	3	AAZ44676	Aaz44676 E. coli s
C 29	21	100.0	1254	4	AAAC91779	Aac91779 Escherich
C 30	21	100.0	1254	10	ADH22653	Adh22653 Escherich
C 31	21	100.0	1259	4	AAH01086	Aah01086 Escherich
C 32	21	100.0	1479	2	AAV11401	Aav11401 Shiga tox
C 33	21	100.0	1612	8	ACA64707	AcA64707 Verotoxin
C 34	21	100.0	1612	10	ADP43307	AdP43307 Superant
C 35	21	100.0	1664	2	AAZ27688	Aaz27688 Verotoxin
C 36	21	100.0	2085	3	AAAS1227	AAAS1227 MBP-VT-2
C 37	21	100.0	2085	6	ABK11958	Abk11958 CDNA enco
C 38	21	100.0	2135	2	AAT42672	Aat42672 Maltose b
C 39	21	100.0	2136	3	AAAS1217	AAAS1217 MBP-VT-2
C 40	21	100.0	2136	6	ABK11798	Abk11798 CDNA enco
C 41	21	100.0	61663	9	ACD19049	Adc19049 E. coli 0
C 42	21	100.0	62708	10	ADCO0199	Adc00199 Enteroha
C 43	21	100.0	134141	6	ABN83487	Abn83487 Escherich
C 44	21	100.0	1234	11	ADL25582	AdL25582 E. coli s
C 45	19.4	92.4	1234	11	ADL25581	AdL25581 E. coli s

ALIGNMENTS

RESULT 1	AAF61481	standard; DNA; 21 BP.
ID	AAF61481	
AC	AAF61481	
DT	18-JUN-2001	(first entry)
DE	EHEC pig pathogen stx2 PCR primer SEQ ID 4.	
DE	EHEC infection; multiplex amplification; detection; human; pig;	
KW	enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; ss.	
OS	Escherichia coli.	
PN	DE19946296-AL.	
PD	23-MAR-2001.	
PF	28-SEP-1999; 99DE-01046296.	
PR	28-SEP-1999; 99DE-01046296.	
PS	(HOF) ROCHER DIAGNOSTICS GMBH.	
PA	Gunzer F, Bellin T;	
PI	WPI; 2001-246145/26.	
PT	Primers for amplifying Shiga toxin sequences in Escherichia coli, useful	
PT	in multiplex amplification detection of enterohemorrhagic strains.	
PS	Claim 1; Page 10; 14pp; German.	
CC	This invention describes a novel primer (P1) which can be used in a	
CC	multiplex amplification reaction for detecting clinically important EHEC	
CC	(enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous	
CC	detection of human and pig pathogens in a single measurement	
XX	Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 21; DB 5; Length 21;	
	Best local Similarity 100.0%; Pred. No. 0.44;	
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 34.0979 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21

Sequence: 1 cgatactccgaagacactg 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	954	3	US-08-816-977-5
2	21	100.0	954	4	US-09-334-477-5
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4	21	100.0	981	4	US-09-334-477-24
5	21	100.0	980	3	US-08-816-977-38
6	21	100.0	990	4	US-09-334-477-38
7	21	100.0	1235	3	US-08-816-977-10
8	21	100.0	1235	4	US-09-334-477-10
9	21	100.0	1254	4	US-09-599-032A-3
10	21	100.0	2085	4	US-08-816-977-48
11	21	100.0	2085	4	US-09-334-477-48
12	21	100.0	2136	3	US-08-816-977-34
13	21	100.0	2136	4	US-09-334-477-34
14	21	100.0	61663	3	US-09-453-702B-62
15	21	100.0	4672	4	US-09-221-017B-846
16	15.8	75.2	4672	4	US-08-956-171E-4332
17	15.4	73.3	366	4	US-08-781-986A-4332
18	15.4	73.3	2933	3	US-08-936-165A-201
19	15.4	73.3	4330	3	US-09-310-293-1
20	15.4	73.3	4330	3	US-09-579-376-1
21	15.4	73.3	14051	4	US-08-956-171E-103
22	15.4	73.3	14051	4	US-08-781-986A-103
23	15.2	72.4	302	4	US-09-702-705-1002
24	15.2	72.4	302	4	US-09-736-457-1002
25	15.2	72.4	302	4	US-09-614-124B-1002
26	15.2	72.4	302	4	US-09-671-325-1002
27	15.2	72.4	302	4	US-09-658-824-1002

28	15.2	72.4	465	4	US-09-248-796A-1824	Sequence 3824, Ap
29	15.2	72.4	555	4	US-09-727-769A-5	Sequence 742, App
30	15.2	72.4	591	4	US-09-540-236-742	Sequence 424, App
31	15.2	72.4	799	3	US-08-998-416-424	Sequence 10330, A
32	15.2	72.4	973	4	US-09-270-767-10330	Sequence 5, App1
33	15.2	72.4	1080	4	US-09-727-769A-7	Sequence 509, Ap
34	15.2	72.4	1188	4	US-09-362-843-5	Sequence 12, App1
35	15.2	72.4	2121	4	US-09-489-039A-5009	Sequence 2, App1
36	15.2	72.4	3348	3	US-09-302-620B-94	Sequence 29, App1
37	15.2	72.4	3348	4	US-08-238-863-84	Sequence 84, App1
38	15.2	72.4	5060	2	US-08-656-555-2	Sequence 28, App
39	15.2	72.4	5062	2	US-08-656-555-1	Sequence 305, App
40	15.2	72.4	66986	4	US-09-596-002-29	
41	15.2	72.4	1230025	4	US-09-198-452A-1	
42	14.8	70.5	81	1	US-08-238-863-84	
43	14.8	70.5	81	5	PCT-US95-05600-228	
44	14.8	70.5	81	5	PCT-US95-05600-228	
45	14.8	70.5	327	4	US-09-270-767-305	

ALIGNMENTS

RESULT 1
US-08-816-977-5/c
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrnes, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSES: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 21; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      100.0%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 48.7113 Seconds
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437.756 Million cell updates/sec

Title: US-10-089-487-5

Perfect score: 30

Sequence: 1 ccgtcacagtaacaacgcgtacatcgctc 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues 1649014

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	30	100.0	969	US-09-334-477-20	Sequence 20, Appl1
5	30	100.0	981	US-08-816-977-36	Sequence 36, Appl1
6	30	100.0	981	US-09-334-477-36	Sequence 36, Appl1
7	30	100.0	1241	US-08-816-977-9	Sequence 9, Appl1
8	30	100.0	1241	US-09-334-477-9	Sequence 9, Appl1
9	30	100.0	2073	US-08-816-977-46	Sequence 46, Appl1
10	30	100.0	2073	US-09-334-477-46	Sequence 46, Appl1
11	30	100.0	2127	US-08-816-977-32	Sequence 32, Appl1
12	30	100.0	2127	US-09-334-477-32	Sequence 32, Appl1
13	30	100.0	48908	US-09-453-7028-137	Sequence 137, Appl1
14	18.6	62.0	1830121	US-09-557-884-1	Sequence 1, Appl1
15	18.6	62.0	1830121	US-09-643-990A-1	Sequence 1, Appl1
16	18.6	62.0	1830121	US-10-329-960-1	Sequence 1, Appl1
17	18.2	60.7	1554	US-09-533-029-91	Sequence 91, Appl1
18	17.8	59.3	1905	US-09-285-744A-1	Sequence 1, Appl1
19	17.8	59.3	6032	US-09-285-744A-12	Sequence 12, Appl1
20	17.4	58.0	2280	US-09-583-110-1146	Sequence 1146, Appl1
21	17.4	58.0	9541	US-08-961-527-132	Sequence 132, Appl1
22	17.2	57.3	954	US-08-816-977-5	Sequence 5, Appl1
23	17.2	57.3	954	US-09-334-477-5	Sequence 5, Appl1
24	17.2	57.3	981	US-08-816-977-24	Sequence 24, Appl1
25	17.2	57.3	981	US-09-334-477-24	Sequence 24, Appl1
26	17.2	57.3	990	US-08-816-977-38	Sequence 38, Appl1
27	17.2	57.3	990	US-09-334-477-38	Sequence 38, Appl1

C 28	17.2	57.3	1235	3	US-08-816-977-10	Sequence 10, Appl1
C 29	17.2	57.3	1235	4	US-09-334-477-10	Sequence 10, Appl1
C 30	17.2	57.3	1254	4	US-09-599-032A-3	Sequence 3, Appl1
C 31	17.2	57.3	1644	4	US-09-248-796A-3594	Sequence 3594, Appl1
C 32	17.2	57.3	2085	3	US-08-816-977-48	Sequence 48, Appl1
C 33	17.2	57.3	2085	4	US-09-334-477-48	Sequence 48, Appl1
C 34	17.2	57.3	2136	3	US-08-816-977-34	Sequence 34, Appl1
C 35	17.2	57.3	2136	4	US-09-334-477-34	Sequence 34, Appl1
C 36	17.2	57.3	3678	4	US-09-112-580-13	Sequence 13, Appl1
C 37	17.2	57.3	50341	1	US-08-247-901C-1	Sequence 1, Appl1
C 38	17.2	57.3	50341	2	US-09-075-904-1	Sequence 1, Appl1
C 39	17.2	57.3	52297	3	US-09-426-436-1	Sequence 1, Appl1
C 40	17.2	57.3	52297	3	US-08-705-557-1	Sequence 1, Appl1
C 41	17.2	57.3	52297	3	US-09-453-7028-62	Sequence 62, Appl1
C 42	17.2	57.3	246240	2	US-08-724-394A-20	Sequence 20, Appl1
C 43	17.2	57.3	246240	2	US-08-724-394A-21	Sequence 21, Appl1
C 44	17.2	57.3	246240	2	US-08-724-394A-22	Sequence 22, Appl1
C 45	17.2	56.7	765	4	US-09-543-681A-919	Sequence 919, Appl1

ALIGNMENTS

RESULT 1
US-08-816-977-1/c
Sequence 1, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M. S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPMD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..945
US-08-816-977-1
Query Match 100.0%; Score 30; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGM note: this result is a transfer of the original file

GenCore version 5.1.6
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Search, using sw model

February 7, 2005, 07:55:37 ; Search time 243.866 Seconds
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US-10-089-487-5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	30	100.0	1241	9	US-09-334-477-9
7	30	100.0	1507	17	US-10-765-580-11
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9	30	100.0	2127	9	US-09-334-477-32
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11	20	66.7	280	9	US-09-294-0938-260
12	20	66.7	284	18	US-10-425-115-152542

13	19.6	65.3	225646	17	US-10-470-565-1	Sequence 1, Appli
14	19.4	64.7	542	18	US-10-425-115-67603	Sequence 67603, A
15	19.4	64.7	589	17	US-10-767-701-580	Sequence 580, App
16	19	63.3	867	17	US-10-437-963-102333	Sequence 102333,
17	19	63.3	1377	17	US-10-437-963-102335	Sequence 102335,
18	18.8	62.7	612	9	US-09-741-669-141	Sequence 141, App
19	18.8	62.7	1171	18	US-10-425-115-69448	Sequence 69448, A
20	18.8	62.7	1263	17	US-10-437-963-32742	Sequence 32742, A
21	18.8	62.7	3609	17	US-10-437-963-32742	Sequence 5611, Ap
22	18.8	62.7	253861	17	US-10-741-601-5611	Sequence 164, App
23	18.8	62.7	261817	13	US-10-087-192-2002	Sequence 2002, Ap
24	18.6	62.0	604	13	US-10-027-632-164	Sequence 164, App
25	18.6	62.0	604	15	US-10-027-632-164	Sequence 164, App
26	18.6	62.0	612	15	US-10-260-238-4520	Sequence 4520, Ap
27	18.6	62.0	717	16	US-10-282-1224-22378	Sequence 22378, A
28	18.6	62.0	858	18	US-10-425-115-7917	Sequence 7917, Ap
29	18.6	62.0	864	18	US-10-425-115-7915	Sequence 7915, Ap
30	18.6	62.0	1199	16	US-10-260-238-4370	Sequence 4370, Ap
31	18.6	62.0	27150	17	US-10-697-828-20	Sequence 20, Appl
32	18.6	62.0	1830121	14	US-10-329-960-1	Sequence 1, Appli
33	18.6	62.0	1830121	16	US-10-329-970-1	Sequence 1, Appli
34	18.6	62.0	1830121	18	US-10-158-865-1	Sequence 190542,
35	18.4	61.3	572	13	US-10-027-632-190542	Sequence 190542,
36	18.4	61.3	572	15	US-10-027-632-190542	Sequence 229, App
37	18.2	60.7	650	10	US-09-854-867-229	Sequence 11641, A
38	18.2	60.7	941	18	US-10-363-345A-11641	Sequence 11642, A
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40	18.2	60.7	1554	15	US-09-533-029-91	Sequence 29, Appl
41	18.2	60.7	1554	15	US-10-278-536-29	Sequence 1103, Ap
42	18.2	60.7	1554	15	US-10-225-066A-1103	Sequence 109, App
43	18.2	60.7	1554	16	US-10-374-780A-109	Sequence 361, App
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ALIGNMENTS

RESULT 1
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; Sequence 93, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Joe
; APPLICANT: BEKAL, Sadia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425, 821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-93

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US-10-765-580-9/c				
; Sequence 9, Application US/10765580				
; Publication No. US2004016555A1				
; GENERAL INFORMATION:				
; APPLICANT: Backer, Marina V.				

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 2064.9 Seconds
(without alignment)
529.417 Million cell updates/sec

Title: US-10-089-487-5

Perfect score: 30
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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8: gb_gg81:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	21.2	70.7	529	8	AZ282444 RPCT-23-1
5	21.2	70.7	773	8	AZ086094 RPCT-23-2
6	20.6	69.3	1055	9	CG882376 ZM8BB049
7	20.6	68.7	521	5	BM300571 BM300571
8	20.6	68.7	638	5	BM170815 BM170815
9	20.2	67.3	586	8	AQ346724 RPCT11-12
10	20.2	67.3	649	1	AV690243 AV690243
11	20.2	66.7	293	4	BI282542 BI282542
12	20	66.7	410	1	A1716987 UI-R-YD0-a
13	20	66.7	432	5	BP015197 BP015197
14	20	66.7	479	2	BF524053 UI-R-YD-a
15	20	66.7	843	9	CNS0477S Tetraodon
16	20	66.7	1020	9	CNS02MMM Tetraodon
17	19.8	66.0	504	8	BZ675685 PUBIH66TD
18	19.8	66.0	772	8	CC446311 PUBH47TD
19	19.6	65.3	466	5	BU086125 SNEST4B03
20	19.6	65.3	702	8	BH056260 RPCT-24-3
21	19.6	65.3	1053	9	CG905026 ZM8BB051
22	19.6	65.3	1101	9	CNS00DB2 Drosophila
23	19.4	64.7	285	2	BE586828 WHE0508 F
24	19.4	64.7	464	2	AMS61714 AMS61714

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27	19.4	64.7	478	6	CB731532
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29	19.4	64.7	499	7	CR465740
30	19.4	64.7	503	7	CN812532
31	19.4	64.7	503	7	CN812533
32	19.4	64.7	589	2	BE360698
33	19.4	64.7	623	4	BU591342
34	19.4	64.7	623	4	AO649119
35	19.4	64.7	650	8	AO649119
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38	19.4	64.7	665	4	BU580557
39	19.4	64.7	667	4	BU608742
40	19.4	64.7	679	8	BH955021
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ALIGNMENTS

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LOCUS 304043 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG384763
VERSION BG384763.1 GI:13309235
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
AUTHORS
Fahrenkrug, S.C., Smith, T.P.L., Fekking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
Quackenbush, J., and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -primatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTACGACG
Plate: 92 row: P column: 18
Seq primer: ATTGAGGACATATAG.

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library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 195.093 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-6
Perfect score: 24
Sequence: 1 tgcacagactgcgtcagtaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	24	100.0	969	9	US-09-334-477-20
5	24	100.0	981	9	US-09-334-477-36
6	24	100.0	1241	9	US-09-334-477-9
7	24	100.0	1507	17	US-10-765-580-11
8	24	100.0	2073	9	US-09-334-477-46
9	24	100.0	2127	9	US-09-334-477-32
10	24	100.0	48908	14	US-10-114-170-137
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12	18.2	75.8	37487	16	US-10-394-948-22

C 13	18.2	75.8	37487	16	US-10-052-482-4	Sequence 4, Appli
C 14	17.6	73.3	154	18	US-10-425-115-16664	Sequence 16664, A
C 15	17.6	73.3	341	16	US-10-424-599-85169	Sequence 85169, A
C 16	17.6	73.3	1217	17	US-10-451-467A-83	Sequence 83, Appli
C 17	17.4	72.5	233	17	US-10-767-701-15871	Sequence 15871, A
C 18	17.4	72.5	611	13	US-10-027-632-189630	Sequence 189630,
C 19	17.4	72.5	611	13	US-10-027-632-189631	Sequence 189631,
C 20	17.4	72.5	611	13	US-10-027-632-189630	Sequence 189630,
C 21	17.4	72.5	611	15	US-10-027-632-189631	Sequence 189631,
C 22	17.2	71.7	567	17	US-10-767-701-26714	Sequence 26714, A
C 23	17.2	71.7	633	13	US-10-027-632-26101	Sequence 26101, A
C 24	17.2	71.7	684	15	US-10-172-118-2169	Sequence 2169, Ap
C 25	17.2	71.7	684	16	US-10-342-887-2169	Sequence 2169, Ap
C 26	17.2	71.7	1519	16	US-10-425-114-26755	Sequence 26755, A
C 27	17.2	71.7	1571	18	US-10-425-115-41305	Sequence 41305, A
C 28	17.2	71.7	10853	18	US-10-723-860-6115	Sequence 6115, Ap
C 29	17.2	71.7	66884	18	US-10-719-993-7036	Sequence 7036, Ap
C 30	17.2	71.7	15554	13	US-10-087-192-391	Sequence 391, App
C 31	17.2	71.7	588	16	US-10-424-599-20612	Sequence 20612, A
C 32	16.8	70.0	1146	9	US-09-429-755-9	Sequence 58838, A
C 33	16.8	70.0	1146	9	US-09-429-755-9	Sequence 9, Appli
C 34	16.8	70.0	1146	9	US-09-429-755-9	Sequence 9, Appli
C 35	16.8	70.0	1146	15	US-10-212-679-9	Sequence 9, Appli
C 36	16.8	70.0	1146	16	US-10-079-137B-9	Sequence 227, App
C 37	16.8	70.0	3646	9	US-09-429-755-227	Sequence 227, App
C 38	16.8	70.0	3646	15	US-10-212-679-227	Sequence 227, App
C 39	16.8	70.0	3646	15	US-10-212-679-227	Sequence 227, App
C 40	16.8	70.0	3646	16	US-10-079-137B-227	Sequence 141, App
C 41	16.8	70.0	3646	15	US-10-212-679-227	Sequence 227, App
C 42	16.8	70.0	3646	16	US-10-079-137B-227	Sequence 141, App
C 43	16.8	70.0	9388	9	US-09-810-936-141	Sequence 141, App
C 44	16.8	70.0	9388	9	US-09-429-755-141	Sequence 141, App
C 45	16.8	70.0	9388	9	US-09-429-755-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-10-425-821-93/c
Sequence 93, Application US/10425821
Publication No. US20040219530A1
GENERAL INFORMATION:
APPLICANT: BROUSSEAU, Roland
APPLICANT: HAREL, Josee
APPLICANT: BEKAL, Sadia
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCE: 86369-3
CURRENT APPLICATION NUMBER: US/10/425, 821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93
LENGTH: 502
TYPE: DNA
ORGANISM: Escherichia coli
US-10-425-821-93

Query Match 100.0%; Score 24; DB 18; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-765-580-9/c
Sequence 9, Application US/10765580
Publication No. US2004016565A1
GENERAL INFORMATION:
APPLICANT: Backer, Marina V.

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 7, 2005, 04:59:52 ; Search time 37.3454 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23
Sequence: 1 agcagaagccttcagcgc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	23	100.0	1235	4	US-08-816-977-10
8	23	100.0	1235	4	US-09-334-477-10
9	23	100.0	1254	4	US-09-599-032A-3
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11	23	100.0	2085	4	US-09-334-477-48
12	23	100.0	2136	4	US-08-816-977-34
13	23	100.0	2136	4	US-09-334-477-34
14	23	100.0	61663	3	US-09-453-702B-62
15	17.2	74.8	2430	2	US-08-820-170A-35
16	17.2	74.8	2430	3	US-09-055-699-35
17	17.2	74.8	2430	3	US-09-273-565-35
18	17.2	74.8	2430	3	US-09-565-538-35
19	17.2	74.8	2430	3	US-09-661-468-35
20	17.2	74.8	2430	4	US-09-976-165-35
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ALIGNMENTS

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C 30	16.6	72.2	1766	3	US-09-058-260-23	Sequence 23, Appl
C 31	16.6	72.2	1896	3	US-09-058-260-3	Sequence 3, Appl
C 32	16.6	72.2	1925	3	US-09-058-260-17	Sequence 17, Appl
C 33	16.6	72.2	1952	3	US-09-058-260-5	Sequence 5, Appl
C 34	16.6	72.2	1957	3	US-09-058-260-19	Sequence 19, Appl
C 35	16.6	72.2	4090	2	US-08-781-802-5	Sequence 5, Appl
C 36	16.6	72.2	4090	3	US-08-694-078-5	Sequence 5, Appl
C 37	16.6	72.2	6263	2	US-08-781-802-3	Sequence 3, Appl
C 38	16.6	72.2	6263	3	US-08-694-078-3	Sequence 3, Appl
C 39	16.2	70.4	12752	2	US-08-459-146-1	Sequence 1, Appl
C 40	16.2	70.4	12752	2	US-08-459-146-1	Sequence 1, Appl
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C 42	15.8	68.7	1830121	4	US-09-643-990A-1	Sequence 1, Appl
C 43	15.8	68.7	1830121	4	US-10-329-960-1	Sequence 1, Appl
C 44	15.6	67.8	885	4	US-09-328-352-3400	Sequence 3400, Ap
C 45	15.6	67.8	1212	4	US-09-489-039A-4710	Sequence 4710, Ap

RESULT 1

US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Rugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPND-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 23; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 186.964 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcagaagccttacgcttcagc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	482	18	US-10-425-821-94
2	23	100.0	954	9	US-09-334-477-5
3	23	100.0	981	9	US-09-334-477-24
4	23	100.0	990	9	US-09-334-477-38
5	23	100.0	1235	9	US-09-334-477-10
6	23	100.0	1612	9	US-09-870-759-27
7	23	100.0	1612	10	US-09-751-708A-27
8	23	100.0	1612	18	US-10-428-817A-23
9	23	100.0	1612	18	US-10-425-821-92
10	23	100.0	2085	9	US-09-334-477-48
11	23	100.0	2136	9	US-09-334-477-34
12	23	100.0	61662	16	US-10-418-837-1

13	23	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl
14	18.2	79.1	543	13	US-10-027-632-48009	Sequence 48009, A
15	18.2	79.1	543	13	US-10-027-632-48010	Sequence 48010, A
16	18.2	79.1	543	15	US-10-027-632-48009	Sequence 48009, A
17	18.2	79.1	543	15	US-10-027-632-48010	Sequence 48010, A
18	18.2	79.1	620	13	US-10-027-632-62196	Sequence 62196, A
19	18.2	79.1	620	13	US-10-027-632-62197	Sequence 62197, A
20	18.2	79.1	620	13	US-10-027-632-62198	Sequence 62198, A
21	18.2	79.1	620	13	US-10-027-632-63111	Sequence 63111, A
22	18.2	79.1	620	13	US-10-027-632-63112	Sequence 63112, A
23	18.2	79.1	620	13	US-10-027-632-64165	Sequence 64165, A
24	18.2	79.1	620	13	US-10-027-632-64166	Sequence 64166, A
25	18.2	79.1	620	13	US-10-027-632-64167	Sequence 64167, A
26	18.2	79.1	620	15	US-10-027-632-62196	Sequence 62196, A
27	18.2	79.1	620	15	US-10-027-632-62197	Sequence 62197, A
28	18.2	79.1	620	15	US-10-027-632-62198	Sequence 62198, A
29	18.2	79.1	620	15	US-10-027-632-63111	Sequence 63111, A
30	18.2	79.1	620	15	US-10-027-632-63112	Sequence 63112, A
31	18.2	79.1	620	15	US-10-027-632-64165	Sequence 64165, A
32	18.2	79.1	620	15	US-10-027-632-64166	Sequence 64166, A
33	18.2	79.1	620	15	US-10-027-632-64167	Sequence 64167, A
34	18.2	79.1	1102	15	US-10-027-632-63110	Sequence 63110, A
35	18.2	79.1	1102	15	US-10-027-632-63111	Sequence 63111, A
36	17.2	74.8	300	18	US-10-425-115-109357	Sequence 109357, A
37	17.2	74.8	642	18	US-10-425-115-63775	Sequence 63775, A
38	17.2	74.8	743	13	US-10-027-632-53457	Sequence 53457, A
39	17.2	74.8	743	15	US-10-027-632-53457	Sequence 53457, A
40	17.2	74.8	1197	18	US-10-425-115-5246	Sequence 5246, Ap
41	17.2	74.8	1421	17	US-10-717-597-60	Sequence 60, Appl
42	17.2	74.8	2430	9	US-09-976-165-35	Sequence 35, Appl
43	17.2	74.8	2430	15	US-10-342-276-35	Sequence 35, Appl
44	17.2	74.8	2977	9	US-09-976-165-35	Sequence 36, Appl
45	17.2	74.8	2977	9	US-09-954-456-735	Sequence 735, App

ALIGNMENTS

RESULT 1
US-10-425-821-94
; Sequence 94, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos'e
; APPLICANT: BEKAL, Sadia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-94

Query Match 100.0%; Score 23; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 414 ACAGAGCCTTACGCTTCAGGC 436

RESULT 2
US-09-334-477-5
; Sequence 5, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 819.794 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagttctgcgtttgtcactgca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	28	100.0	963	CFSLTITICA	Sequence
5	28	100.0	981	AR099878	Sequence
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7	28	100.0	990	AR099887	Sequence
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10	28	100.0	1220	AB048835	Sequence
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13	28	100.0	1224	AB048239	Sequence
14	28	100.0	1235	AR099867	Sequence
15	28	100.0	1235	AR431401	Sequence
16	28	100.0	1236	ECED42SLT	Sequence
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20	28	100.0	1237	1	AB048240	Escherich
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ALIGNMENTS

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DEFINITION	AX106739					
ACCESSION	AX106739.1	GI:13922400				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
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Query Match						
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RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
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SOURCE						
ORGANISM						
Unclassified.						

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 227.608 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagcttcgcttcgttcactgca 28

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	482	18	US-10-425-821-94
2	28	100.0	954	9	US-09-334-477-5
3	28	100.0	981	9	US-09-334-477-24
4	28	100.0	990	9	US-09-334-477-38
5	28	100.0	1235	9	US-09-334-477-10
6	28	100.0	1612	9	US-09-870-759-27
7	28	100.0	1612	10	US-09-751-708A-27
8	28	100.0	1612	18	US-10-428-817A-23
9	28	100.0	1612	18	US-10-425-821-92
10	28	100.0	2085	9	US-09-334-477-48
11	28	100.0	2136	9	US-09-334-477-34
12	28	100.0	61662	16	US-10-418-837-1

13	28	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl
14	24	85.7	39	14 <td>US-10-085-056-35</td> <td>Sequence 35, Appl</td>	US-10-085-056-35	Sequence 35, Appl
15	20.6	73.6	1030	9 <td>US-09-945-376-3</td> <td>Sequence 3, Appl</td>	US-09-945-376-3	Sequence 3, Appl
16	20	71.4	1323	15 <td>US-10-369-493-32410</td> <td>Sequence 3410, A</td>	US-10-369-493-32410	Sequence 3410, A
17	19.2	68.6	47443	11 <td>US-09-997-722-94</td> <td>Sequence 94, Appl</td>	US-09-997-722-94	Sequence 94, Appl
18	19	67.9	474	13 <td>US-10-027-632-129849</td> <td>Sequence 129849, A</td>	US-10-027-632-129849	Sequence 129849, A
19	19	67.9	474	15 <td>US-10-027-632-129849</td> <td>Sequence 129849, A</td>	US-10-027-632-129849	Sequence 129849, A
20	19	67.9	13440	15 <td>US-10-213-848-12</td> <td>Sequence 12, Appl</td>	US-10-213-848-12	Sequence 12, Appl
21	18.6	66.4	444	18 <td>US-10-357-930-13108</td> <td>Sequence 1108, A</td>	US-10-357-930-13108	Sequence 1108, A
22	18.4	65.7	113	15 <td>US-10-029-586-26028</td> <td>Sequence 26028, A</td>	US-10-029-586-26028	Sequence 26028, A
23	18.4	65.7	505	15 <td>US-10-425-115-11289</td> <td>Sequence 11289, A</td>	US-10-425-115-11289	Sequence 11289, A
24	18.4	65.7	568	15 <td>US-10-029-386-12328</td> <td>Sequence 12328, A</td>	US-10-029-386-12328	Sequence 12328, A
25	18.4	65.7	640	13 <td>US-10-027-632-137774</td> <td>Sequence 137774, A</td>	US-10-027-632-137774	Sequence 137774, A
26	18.4	65.7	640	13 <td>US-10-027-632-137774</td> <td>Sequence 137774, A</td>	US-10-027-632-137774	Sequence 137774, A
27	18.4	65.7	774	13 <td>US-10-027-632-137773</td> <td>Sequence 137773, A</td>	US-10-027-632-137773	Sequence 137773, A
28	18.4	65.7	774	15 <td>US-10-027-632-137773</td> <td>Sequence 137773, A</td>	US-10-027-632-137773	Sequence 137773, A
29	18.4	65.7	1161	16 <td>US-10-425-114-29267</td> <td>Sequence 29267, A</td>	US-10-425-114-29267	Sequence 29267, A
30	18.4	65.7	1161	18 <td>US-10-425-115-143253</td> <td>Sequence 143253, A</td>	US-10-425-115-143253	Sequence 143253, A
31	18.2	65.0	2385	16 <td>US-10-282-122A-32403</td> <td>Sequence 32403, A</td>	US-10-282-122A-32403	Sequence 32403, A
32	18.2	65.0	3106	13 <td>US-10-027-632-113748</td> <td>Sequence 113748, A</td>	US-10-027-632-113748	Sequence 113748, A
33	18.2	65.0	3106	15 <td>US-10-027-632-113748</td> <td>Sequence 113748, A</td>	US-10-027-632-113748	Sequence 113748, A
34	18	64.3	5885	16 <td>US-10-062-674-11770</td> <td>Sequence 11770, Ap</td>	US-10-062-674-11770	Sequence 11770, Ap
35	18	64.3	83719	17 <td>US-10-388-838-45</td> <td>Sequence 45, Appl</td>	US-10-388-838-45	Sequence 45, Appl
36	18	64.3	197997	9 <td>US-09-822-246-3</td> <td>Sequence 3, Appl</td>	US-09-822-246-3	Sequence 3, Appl
37	18	64.3	197997	18 <td>US-10-469-028-3</td> <td>Sequence 3, Appl</td>	US-10-469-028-3	Sequence 3, Appl
38	18	64.3	684187	17 <td>US-10-367-094-71</td> <td>Sequence 71, Appl</td>	US-10-367-094-71	Sequence 71, Appl
39	17.8	63.6	448	10 <td>US-09-918-995-35148</td> <td>Sequence 35148, A</td>	US-09-918-995-35148	Sequence 35148, A
40	17.8	63.6	3833	15 <td>US-10-104-047-339</td> <td>Sequence 339, App</td>	US-10-104-047-339	Sequence 339, App
41	17.8	63.6	4816	18 <td>US-10-357-930-23466</td> <td>Sequence 23466, A</td>	US-10-357-930-23466	Sequence 23466, A
42	17.6	62.9	4816	18 <td>US-10-357-930-29353</td> <td>Sequence 29353, A</td>	US-10-357-930-29353	Sequence 29353, A
43	17.6	62.9	405	9 <td>US-09-918-995-3446</td> <td>Sequence 3446, Ap</td>	US-09-918-995-3446	Sequence 3446, Ap
44	17.6	62.9	407	9 <td>US-09-764-877-667</td> <td>Sequence 667, App</td>	US-09-764-877-667	Sequence 667, App
45	17.6	62.9	407	16 <td>US-10-242-515-667</td> <td>Sequence 667, App</td>	US-10-242-515-667	Sequence 667, App

ALIGNMENTS

RESULT 1
US-10-425-821-94
Sequence 94, Application US/10425821
Publication No. US20040219530A1
GENERAL INFORMATION:
APPLICANT: BROUSSEAU, Roland
APPLICANT: BEKEL, Jos'e
APPLICANT: BEKEL, Sadi'a
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCE: 86369-3
CURRENT APPLICATION NUMBER: US/10/425,821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn version 3.2
SEQ ID NO 94
LENGTH: 482
TYPE: DNA
ORGANISM: Escherichia coli
US-10-425-821-94

Query Match 100.0%; Score 28; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGCAGTTCGCTTCGTTGTCACGTGCA 28
DB 385 AGAGCAGTTCGCTTCGTTGTCACGTGCA 412

RESULT 2
US-09-334-477-5
Sequence 5, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 614.845 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21
Sequence: 1 CGATCTCCGAGACATG 21

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:.*
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14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	21	100.0	954	6	AR431398 Sequence
4	21	100.0	963	1	CFSLTICA
5	21	100.0	981	6	AR099878 Sequence
6	21	100.0	981	6	AR431412 Sequence
7	21	100.0	990	6	AR099887 Sequence
8	21	100.0	990	6	AR431421 Sequence
9	21	100.0	1220	1	AB048835
10	21	100.0	1220	1	AB048836
11	21	100.0	1224	1	AB048837
12	21	100.0	1235	6	AR09867 Sequence
13	21	100.0	1235	6	AR431401
14	21	100.0	1236	1	ECED42ST
15	21	100.0	1236	1	ECED43SLT
16	21	100.0	1236	1	ECED43SLT
17	21	100.0	1236	1	ECED68SLT
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19	21	100.0	1237	1	AB048240

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C 21	21	100.0	1241	1	EC0272135	AJ272135 Escherich
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C 25	21	100.0	1241	7	AY633454	AY633454 Bacteriop
C 26	21	100.0	1241	7	AY633455	AY633455 Bacteriop
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ALIGNMENTS

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ACCESSION	AX106736				
VERSION	AX106736.1	GI:13922397			
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FEATURES					
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LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
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LOCUS	AR099864	Sequence 5 from patent US 6080400.			
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TITLE					

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 585.567 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-3

Perfect score: 20

Sequence: 1 ttccggatgcgaatcagtc 20

Scoring table:

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	152	7 BF5251233	BF5251233 Bacterioph
5	20	100.0	153	7 BF3251232	BF3251232 Bacterioph
6	20	100.0	157	7 BF1251231	BF1251231 Bacterioph
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8	20	100.0	296	1 ECUA1240	ECUA1240 Escherichia
9	20	100.0	298	1 ECUA1236	ECUA1236 Escherichia
10	20	100.0	298	1 ECUA1238	ECUA1238 Escherichia
11	20	100.0	299	1 ECUA1235	ECUA1235 Escherichia
12	20	100.0	307	1 ECUA1242	ECUA1242 Escherichia
13	20	100.0	310	1 ECUA1239	ECUA1239 Escherichia
14	20	100.0	312	1 ECUA1237	ECUA1237 Escherichia
15	20	100.0	320	1 ECUA1243	ECUA1243 Escherichia
16	20	100.0	329	1 ECUA1244	ECUA1244 Escherichia
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19	20	100.0	439	1 AB119452	AB119452 Escherich

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29	20	100.0	515	1	AF532128	AF532128 Escherich
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31	20	100.0	540	6	E66923	E66923 Method for
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33	20	100.0	954	6	AR099864	AR099864 Sequence
34	20	100.0	954	6	AR431398	AR431398 Sequence
35	20	100.0	963	1	CRSLTICA	X67514 C firendli
36	20	100.0	981	6	AR099878	AR099878 Sequence
37	20	100.0	981	6	AR431412	AR431412 Sequence
38	20	100.0	990	6	AR099887	AR099887 Sequence
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ALIGNMENTS

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

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Sequence 3 from Patent WO0123607.
AX106735
AX106735.1 GI:13922396
Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

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Gruner, F. and Bellin, T.
Multiplex PCR for detecting ehc infections
Patent: WO 0123607-A 3 05-APR-2001;
Roche Diagnostics GmbH (DE)
Location/Qualifiers
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DB 1 TTCCGGATGCATCAGTC 20

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KEYWORDS
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Sequence 7 from Patent WO03010332.
AX698158
AX698158.1 GI:29499167

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synthetic construct
artificial sequences.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
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1615.176 Million cell updates/sec

Title: US-10-089-487-2
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Searched: 4526729 seqs, 2364489745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	24	100.0	969	AR431410 Sequence
7	24	100.0	981	AR099886 Sequence
8	24	100.0	981	AR431420 Sequence
9	24	100.0	1238	AB015056 Sequence
10	24	100.0	1238	AB030485 Sequence
11	24	100.0	1238	AB048232 Sequence
12	24	100.0	1241	AR099866 Sequence
13	24	100.0	1241	AR431400 Sequence
14	24	100.0	1297	AB035142 Sequence
15	24	100.0	1320	SDFOXAB
16	24	100.0	1362	SS0132761
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18	24	100.0	1433	ECSLTABA
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c 21	24	100.0	1500	1	SHPSHT	M19437 S.dysenteri
c 22	24	100.0	1591	7	H19BSLT	M16625 Bacterioph
c 23	24	100.0	1601	1	AF461166	AF461166 Escherich
c 24	24	100.0	1601	1	AF461168	AF461168 Escherich
c 25	24	100.0	1601	1	AF461169	AF461169 Escherich
c 26	24	100.0	1710	7	H19BSLT	M17358 Bacterioph
c 27	24	100.0	1905	7	H30SLT	M23980 Bacterioph
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c 31	24	100.0	2127	6	AR099884	AR099884 Sequence
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c 33	24	100.0	2540	1	AB083043	AB083043 Escherich
c 34	24	100.0	3294	1	SHPSHT	M23352 S.dysenteri
c 35	24	100.0	5467	1	ECO251325	ECO251325 Escherich
c 36	24	100.0	5567	1	ECOSLTI	L04539 Escherich
c 37	24	100.0	6014	1	SDY271153	AJ771153 Shigella
c 38	24	100.0	6921	7	ECO413275	AJ771153 Bacterioph
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c 40	24	100.0	10127	1	AE005442	AE005442 Escherich
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DEFINITION Sequence 2 from Patent WO0123607.
ACCESSION AX106734
VERSION AX106734.1 GI:13922395

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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE
AUTHORS
TITLE
JOURNAL
1
Gunzer, F. and Bellin, T.
Multiplex PCR for detecting ehc infections
Patent: WO 0123607-A 2 05-APR-2001;
Roche Diagnostics GmbH (DE)

FEATURES
Location/Qualifiers

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Db 1 CCGACACATGAGGAATCAT 24
RESULT 2
LOCUS AR099862/c 945 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6080400.
ACCESSION AR099862
VERSION AR099862.1 GI:12810310
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 184.701 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24

Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapect 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: Geneseq19808:*
- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20018:*
- 6: Geneseq20028:*
- 7: Geneseq20028:*
- 8: Geneseq20038:*
- 9: Geneseq20038:*
- 10: Geneseq20038:*
- 11: Geneseq20038:*
- 12: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	24	5	AA61483	Aa61483 EHEC huma
2	100.0	43	2	AAT97605	Aat97605 Shigella
3	100.0	287	12	ADN02037	Adn02037 Enterohae
4	100.0	870	10	AD14887	Ad14887 DNA encod
5	100.0	945	2	AAT42649	Aat42649 Verotoxig
6	100.0	945	2	AA51194	AA51194 E. coli v
7	100.0	945	6	ABK11775	Abk11775 E. coli v
8	100.0	948	4	AAH01085	Aah01085 Escherich
9	100.0	969	2	AAT42663	Aat42663 Histeridine
10	100.0	969	3	AA51208	AA51208 Recombina
11	100.0	969	6	ABK11789	Abk11789 CDNA enco
12	100.0	980	2	AAT42673	Aat42673 FLAG tag/
13	100.0	981	6	AA51218	AA51218 FLAG tag-
14	100.0	1192	2	AAV11402	Aav11402 Shiga tox
15	100.0	1207	2	AAV11403	Aav11403 Shiga tox
16	100.0	1227	11	AD125576	Ad125576 S. dysent
17	100.0	1227	11	AD125577	Ad125577 S. sonnei
18	100.0	1227	11	AD125578	Ad125578 Bacteriop
19	100.0	1230	2	AAQ12711	Aaq12711 Shiga-11k
20	100.0	1230	2	AAQ12711	Aaq12711 Shiga-11k
21	100.0	1230	2	AAT91637	Aat91637 Phage H19

C 22	24	100.0	1230	2	AA230662	Aa230662 E.coli ba
C 23	24	100.0	1230	3	AA290018	Aa290018 E. coli b
C 24	24	100.0	1235	2	AAV11404	Aav11404 Shiga tox
C 25	24	100.0	1241	2	AAT42653	Aat42653 Sequence
C 26	24	100.0	1241	6	AA51198	AA51198 DNA direc
C 27	24	100.0	1241	6	ABK11779	Abk11779 Polyclistr
C 28	24	100.0	1369	2	AA227687	Aa227687 Verotoxin
C 29	24	100.0	1389	2	AAV11400	Aav11400 Shiga tox
C 30	24	100.0	2073	6	AA51226	AA51226 MBP-VT-1
C 31	24	100.0	2073	6	ABK11957	Abk11957 CDNA enco
C 32	24	100.0	2126	2	AAT42671	Aat42671 Maltose b
C 33	24	100.0	2127	3	AA51216	AA51216 MBP-VT-1
C 34	24	100.0	2127	6	ABK11797	Abk11797 CDNA enco
C 35	24	100.0	47879	10	ADC00509	Adc00509 Enterohae
C 36	24	100.0	48908	9	ACD19124	Ac19124 E. coli 0
C 37	18.2	80.0	1188	12	ADU75891	Ad75891 Marker ge
C 38	18.2	75.8	37487	9	ADA02498	Ada02498 Human MYC
C 39	18.2	75.8	37487	10	ADB72236	Ad72236 Human MYC
C 40	18.2	75.8	37487	10	ADE82938	Ad82938 Human MYC
C 41	18.2	75.8	37487	10	ADE95746	Ad95746 Human MYC
C 42	17.6	73.3	1217	6	ABQ76329	Abq76329 S. cerevi
C 43	17.6	73.3	1687	4	AB118110	Ab118110 Drosophi1
C 44	17.6	73.3	1687	4	AB112468	Ab112468 Drosophi1
C 45	17.6	73.3	1687	4	AB118210	Ab118210 Drosophi1

ALIGNMENTS

RESULT 1
AA61483
ID AA61483 standard; DNA; 24 BP.

AC AA61483;
DT 18-JUN-2001 (first entry)

DE EHEC human pathogen strA1 probe SEQ ID 6.

KW EHEC infection; multiplex amplification; detection; human; pig;
enterohemorrhagic Escherichia coli infection; pathogen; probe; ss.

OS Escherichia coli.

FN DE19946296-A1.

PD 29-MAR-2001.

PF 28-SEP-1999; 99DE-01046296.

PR 28-SEP-1999; 99DE-01046296.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PI Gunzer F, Bellin T;
WPI; 2001-246145/26.

PT Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
in multiplex amplification detection of enterohemorrhagic strains.

PS Claim 11; Page 10; 14pp; German.

CC This invention describes a novel primer (PI) which can be used in a
multiplex amplification reaction for detecting clinically important EHEC
(enterohemorrhagic Escherichia coli) infections. PI allow simultaneous
detection of human and pig pathogens in a single measurement

SO Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-1

Sequence: 1 agtcgtacggggatgcagataaat 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6 AX106733	AX106733 Sequence
2	24	100.0	39	6 AX524899	AX524899 Sequence
3	24	100.0	39	6 BD174563	BD174563 Oligonucleotide
4	24	100.0	945	6 AR099862	AR099862 Sequence
5	24	100.0	945	6 AR431396	AR431396 Sequence
6	24	100.0	948	1 AB071619	AB071619 Escherichia coli
7	24	100.0	948	1 AB071621	AB071621 Escherichia coli
8	24	100.0	948	1 AB071623	AB071623 Escherichia coli
9	24	100.0	948	6 AX110343	AX110343 Sequence
10	24	100.0	969	6 AR099876	AR099876 Sequence
11	24	100.0	969	6 AR431410	AR431410 Sequence
12	24	100.0	981	6 AR099886	AR099886 Sequence
13	24	100.0	981	6 AR431420	AR431420 Sequence
14	24	100.0	1227	1 AB083044	AB083044 Escherichia coli
15	24	100.0	1238	1 AB015056	AB015056 Escherichia coli
16	24	100.0	1238	1 AB030485	AB030485 Escherichia coli
17	24	100.0	1238	1 AB048232	AB048232 Escherichia coli
18	24	100.0	1238	1 AB048235	AB048235 Escherichia coli
19	24	100.0	1239	1 AB048231	AB048231 Escherichia coli

20	24	100.0	1239	1 AB048237	AB048237 Escherichia coli
21	24	100.0	1240	1 AB048234	AB048234 Escherichia coli
22	24	100.0	1241	6 AR099866	AR099866 Sequence
23	24	100.0	1241	6 AR431400	AR431400 Sequence
24	24	100.0	1271	1 AY170851	AY170851 Escherichia coli
25	24	100.0	1297	1 AB035142	AB035142 Escherichia coli
26	24	100.0	1330	1 SDTOXAB	X07903 Shigella dysenteriae
27	24	100.0	1338	1 AY135685	AY135685 Escherichia coli
28	24	100.0	1362	1 SSO132761	SSO132761 Shigella
29	24	100.0	1369	6 E27911	E27911 Method for
30	24	100.0	1414	7 B62413986	B62413986 Bacteriophage
31	24	100.0	1432	1 ECO312232	ECO312232 Escherichia coli
32	24	100.0	1432	1 ECO314838	ECO314838 Escherichia coli
33	24	100.0	1432	1 ECO314839	ECO314839 Escherichia coli
34	24	100.0	1433	1 ECSLTIAB	ECSLTIAB Escherichia coli
35	24	100.0	1433	1 ECSLTIAB	ECSLTIAB Escherichia coli
36	24	100.0	1434	1 ECSLTIAB	ECSLTIAB Escherichia coli
37	24	100.0	1499	7 J93SLTI	J93SLTI Escherichia coli
38	24	100.0	1500	7 SHFSHT	SHFSHT Escherichia coli
39	24	100.0	1591	7 H19BSLT	H19BSLT Escherichia coli
40	24	100.0	1601	1 AF461166	AF461166 Escherichia coli
41	24	100.0	1601	1 AF461168	AF461168 Escherichia coli
42	24	100.0	1601	1 AF461169	AF461169 Escherichia coli
43	24	100.0	1650	1 AB050958	AB050958 Escherichia coli
44	24	100.0	1650	1 AB050959	AB050959 Escherichia coli
45	24	100.0	1710	7 H19BSLT	H19BSLT Bacteriophage

ALIGNMENTS

RESULT 1	AX106733	Sequence 1 from Patent WO0123607.	24 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106733					
DEFINITION	AX106733					
ACCESSION	AX106733					
VERSION	AX106733.1	GI:13922394				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Qy						
Db						
RESULT 2	AX524899	Sequence 28 from Patent EP1236806.	39 bp	DNA	linear	PAT 21-NOV-2002
LOCUS	AX524899					
DEFINITION	AX524899					
ACCESSION	AX524899					
VERSION	AX524899.1	GI:25169986				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Qy						
Db						

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 878.351 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-5
Perfect score: 30
Sequence: 1 ctgtcacagtaacacgcgtacatcgctc 30

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 4526729 seqs, 2364489745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ha: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sls: *
12: gb_gy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	6	AX106737 Sequence
2	30	100.0	945	6	AR099862 Sequence
3	30	100.0	945	6	AR431396 Sequence
4	30	100.0	948	1	AB071623 Sequence
5	30	100.0	948	6	AX110343 Sequence
6	30	100.0	969	6	AR099876 Sequence
7	30	100.0	969	6	AR431410 Sequence
8	30	100.0	981	6	AR099886 Sequence
9	30	100.0	981	6	AR431420 Sequence
10	30	100.0	1227	1	AB083044 Escherich
11	30	100.0	1238	1	AB015056 Escherich
12	30	100.0	1238	1	AB030485 Escherich
13	30	100.0	1238	1	AB048232 Escherich
14	30	100.0	1238	1	AB048235 Escherich
15	30	100.0	1239	1	AB048231 Escherich
16	30	100.0	1239	1	AB048237 Escherich
17	30	100.0	1240	1	AB048234 Escherich
18	30	100.0	1241	6	AR099866 Sequence
19	30	100.0	1241	6	AR431400 Sequence

c 20	30	100.0	1297	1	AB035142 Escherich
c 21	30	100.0	1320	1	SDTOXAB X07903 Shigella dy
c 22	30	100.0	1338	1	AY135685 Escherich
c 23	30	100.0	1362	1	SS0132761 Shigella
c 24	30	100.0	1369	6	E27911 Method for
c 25	30	100.0	1414	7	B62413986 Bacteriop
c 26	30	100.0	1432	1	ECO312232 Escherich
c 27	30	100.0	1432	1	ECO314838 Escherich
c 28	30	100.0	1432	1	ECO314839 Escherich
c 29	30	100.0	1433	1	EC0314839 Escherich
c 30	30	100.0	1433	1	EC0314839 Escherich
c 31	30	100.0	1434	1	EC0314839 Escherich
c 32	30	100.0	1499	7	J93SLT1 Bacterioph
c 33	30	100.0	1500	1	SHRSMT M1437 S.dysenter
c 34	30	100.0	1591	7	H19BSLT1 M1625 Bacterioph
c 35	30	100.0	1601	1	AF461166 Escherich
c 36	30	100.0	1601	1	AF461168 Escherich
c 37	30	100.0	1601	1	AF461169 Escherich
c 38	30	100.0	1710	7	H19BSLT1 M17358 Bacterioph
c 39	30	100.0	1905	7	H30SLT1 M23980 Bacterioph
c 40	30	100.0	1956	1	AF461172 Escherich
c 41	30	100.0	2073	6	AR099894 Sequence
c 42	30	100.0	2073	6	AR431428 Sequence
c 43	30	100.0	2127	6	AR099884 Sequence
c 44	30	100.0	2127	6	AR431418 Sequence
c 45	30	100.0	2540	1	AB083043 Escherich

ALIGNMENTS

RESULT 1	AX106737	Sequence 5 from Patent WO0123607.	30 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106737					
DEFINITION	Sequence 5 from Patent WO0123607.					
ACCESSION	AX106737					
VERSION	AX106737.1	GI:13922398				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE	1	Gunzer, F. and Bellin, T.				
AUTHORS						
TITLE		Multiplex PCR for detecting ehc infections				
JOURNAL		Patent: WO 0123607-A 5 05-APR-2001;				
FEATURES		Roche Diagnostics GmbH (DE)				
SOURCE		Location/Qualifiers				
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		/organism="Escherichia coli"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:562"				
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Best Local Similarity		100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;				
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OR	1	CTGTACAGTACAAACCGTACATCGCTC 30				
DB	1	CTGTACAGTACAAACCGTACATCGCTC 30				
RESULT 2	AR099862/c	945 bp	DNA	linear	PAT 14-FEB-2001	
LOCUS	AR099862					
DEFINITION	Sequence 1 from patent US 6080400.					
ACCESSION	AR099862					
VERSION	AR099862.1	GI:12810310				
KEYWORDS						
SOURCE						
ORGANISM						
		Unknown.				
		Unclassified.				

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24
Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	24	100.0	24	AX106738 Sequence
2	24	100.0	43	AR019038 Sequence
3	24	100.0	945	AR099862 Sequence
4	24	100.0	945	AR431396 Sequence
5	24	100.0	948	AB071619 Escherich
6	24	100.0	948	AB071621 Escherich
7	24	100.0	948	AB071623 Escherich
8	24	100.0	948	AX110343 Sequence
9	24	100.0	969	AR099876 Sequence
10	24	100.0	969	AR431410 Sequence
11	24	100.0	981	AR099886 Sequence
12	24	100.0	981	AR431420 Sequence
13	24	100.0	1227	AB083044 Escherich
14	24	100.0	1238	AB015056 Escherich
15	24	100.0	1238	AB030485 Escherich
16	24	100.0	1238	AB048232 Escherich
17	24	100.0	1238	AB048235 Escherich
18	24	100.0	1239	AB048231 Escherich
19	24	100.0	1239	AB048237 Escherich

C 20	24	100.0	1240	1	AB048234 Escherich
C 21	24	100.0	1241	6	AR099866 Sequence
C 22	24	100.0	1241	6	AR431400 Sequence
C 23	24	100.0	1297	1	AB035142 Escherich
C 24	24	100.0	1320	1	SDTOXAB
C 25	24	100.0	1338	1	AV135685 Escherich
C 26	24	100.0	1362	1	SS0132761
C 27	24	100.0	1369	6	E27911 Method for
C 28	24	100.0	1414	7	B62413986
C 29	24	100.0	1432	1	EC0312232
C 30	24	100.0	1432	1	EC0314838
C 31	24	100.0	1432	1	EC0314839
C 32	24	100.0	1433	1	EC0314839
C 33	24	100.0	1433	1	EC0314839
C 34	24	100.0	1434	1	EC0314839
C 35	24	100.0	1499	7	J93SLTI
C 36	24	100.0	1500	1	SHFSHT
C 37	24	100.0	1591	7	H19BSLT
C 38	24	100.0	1601	1	AF461166
C 39	24	100.0	1601	1	AF461168
C 40	24	100.0	1601	1	AF461169
C 41	24	100.0	1710	7	H19BSLT
C 42	24	100.0	1905	7	H30SLT
C 43	24	100.0	1956	1	AF461172
C 44	24	100.0	2073	6	AR099894
C 45	24	100.0	2073	6	AR431428

ALIGNMENTS

RESULT 1
AX106738 24 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 6 from Patent WO0123607.
AX106738
AX106738.1 GI:13922399

REFERENCE
AUTHORS Gunzer, F. and Bellin, T.
TITLE Multiplex PCR for detecting ehc infections
JOURNAL Patent: WO 0123607-A 6 05-APR-2001;
Roche Diagnostics GmbH (DE)
FEATURES
source location/Qualifiers
1..24
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"

ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TGCACAGACTGCCTCAGTGAGGT 24
DB 1 TGCACAGACTGCCTCAGTGAGGT 24

RESULT 2
AR019038/c 43 bp DNA linear PAT 05-DEC-1998
LOCUS AR019038 Sequence 18 from patent US 5783196.
DEFINITION AR019038
ACCESSION AR019038
VERSION AR019038.1 GI:3974152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
Unclassified.

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 38.9691 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24
Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	100.0	43	1	US-08-629-600-18
C 2	24	100.0	945	3	US-08-816-977-1
C 3	24	100.0	945	4	US-09-334-477-1
C 4	24	100.0	969	3	US-08-816-977-20
C 5	24	100.0	969	4	US-09-334-477-20
C 6	24	100.0	981	3	US-08-816-977-36
C 7	24	100.0	981	4	US-09-334-477-36
C 8	24	100.0	1241	4	US-08-816-977-9
C 9	24	100.0	1241	3	US-09-334-477-9
C 10	24	100.0	2073	4	US-08-816-977-46
C 11	24	100.0	2073	3	US-09-334-477-46
C 12	24	100.0	2127	4	US-08-816-977-32
C 13	24	100.0	2127	3	US-09-334-477-32
C 14	24	100.0	48908	4	US-09-453-702B-137
C 15	17.2	71.7	859	3	US-09-976-594-499
C 16	16.8	70.0	1146	3	US-08-991-789A-9
C 17	16.8	70.0	1146	4	US-09-662-451-9
C 18	16.8	70.0	1146	3	US-09-598-326-9
C 19	16.8	70.0	1146	4	US-09-289-198-9
C 20	16.8	70.0	1146	3	US-09-429-755-9
C 21	16.8	70.0	3646	3	US-08-991-789A-227
C 22	16.8	70.0	3646	4	US-09-662-451-227
C 23	16.8	70.0	3646	3	US-09-598-326-227
C 24	16.8	70.0	3646	4	US-09-289-198-227
C 25	16.8	70.0	3646	3	US-09-429-755-227
C 26	16.8	70.0	3646	4	US-08-991-789A-141
C 27	16.8	70.0	9388	3	US-09-062-451-141

C 28	16.8	70.0	9388	4	US-09-598-326-141	Sequence 141, App
C 29	16.8	70.0	9388	4	US-09-289-198-141	Sequence 141, App
C 30	16.8	70.0	9388	4	US-09-429-755-141	Sequence 141, App
C 31	16.8	70.0	75395	4	US-09-984-890-3	Sequence 3, Appl
C 32	16.8	70.0	75395	4	US-10-274-194-3	Sequence 3, Appl
C 33	16.6	69.2	444	4	US-09-270-767-2199	Sequence 2199, App
C 34	16.6	69.2	444	4	US-09-270-767-17481	Sequence 17481, App
C 35	16.6	69.2	539	4	US-09-513-999C-10940	Sequence 10940, A
C 36	16.6	69.2	1776	4	US-09-489-039A-3634	Sequence 3634, A
C 37	16.6	69.2	4371	1	US-08-803-972-1	Sequence 1, Appl
C 38	16.6	69.2	4371	1	US-08-803-972-1	Sequence 1, Appl
C 39	16.4	68.3	168174	4	US-10-071-411A-63	Sequence 63, Appl
C 40	16.4	68.3	168273	4	US-10-071-411A-2	Sequence 2, Appl
C 41	16.2	67.5	336	4	US-09-513-999C-24032	Sequence 24032, A
C 42	16.2	67.5	627	4	US-09-270-767-12248	Sequence 12248, A
C 43	16.2	67.5	4792	3	US-08-781-891-205	Sequence 205, App
C 44	16.2	67.5	4792	4	US-09-618-166-205	Sequence 205, App
C 45	16.2	67.5	6476	3	US-09-127-670-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-629-600-18/c
Sequence 18, Application US/08629600
Patent No. 5783196

GENERAL INFORMATION:
APPLICANT: NORIEGA, Fernando
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-629-600-18

Query Match 100.0% ; Score 24 ; DB 1 ; Length 43 ;
Best Local Similarity 100.0% ; Pred. No. 0.028 ;
Matches 24 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 1 TGCACAGACTGCGTCAGTGAGGT 24
DB 37 TGCACAGACTGCGTCAGTGAGGT 14

Fri Feb 11 08:08:37 2005

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 673.402 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcagaagccttacgcttcagc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb da:*

2: gb htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	6	AX106740 Sequence
2	23	100.0	954	6	AR099864 Sequence
3	23	100.0	954	6	AR431398 Sequence
4	23	100.0	954	1	AR099878 Sequence
5	23	100.0	981	6	AR431412 Sequence
6	23	100.0	981	6	AR099887 Sequence
7	23	100.0	990	6	AR431421 Sequence
8	23	100.0	1220	1	AB048835 Escherich
9	23	100.0	1220	1	AB048836 Escherich
10	23	100.0	1220	1	AB048837 Escherich
11	23	100.0	1224	1	AB048239 Escherich
12	23	100.0	1235	6	AR099867 Sequence
13	23	100.0	1235	6	AR431401 Sequence
14	23	100.0	1237	1	AB048240 Escherich
15	23	100.0	1241	1	AB048233 Escherich
16	23	100.0	1241	6	E03959 The VT2 gen
17	23	100.0	1241	6	E03962 The VT2 gen
18	23	100.0	1241	7	AY633453 Bacteriop
19	23	100.0	1241	7	AY633453 Bacteriop

20	23	100.0	1241	7	AY633454 Bacteriop
21	23	100.0	1241	7	AY633455 Bacteriop
22	23	100.0	1241	7	AY633456 Bacteriop
23	23	100.0	1241	7	AY633457 Bacteriop
24	23	100.0	1241	7	AY633458 Bacteriop
25	23	100.0	1241	7	AY633459 Bacteriop
26	23	100.0	1241	7	AY633460 Bacteriop
27	23	100.0	1241	7	AY633461 Bacteriop
28	23	100.0	1241	7	AY633462 Bacteriop
29	23	100.0	1241	7	AY633463 Bacteriop
30	23	100.0	1241	7	AY633464 Bacteriop
31	23	100.0	1241	7	AY633465 Bacteriop
32	23	100.0	1241	7	AY633466 Bacteriop
33	23	100.0	1241	7	AY633467 Bacteriop
34	23	100.0	1241	7	AY633468 Bacteriop
35	23	100.0	1241	7	AY633469 Bacteriop
36	23	100.0	1241	7	AY633470 Bacteriop
37	23	100.0	1241	7	AY633471 Bacteriop
38	23	100.0	1241	7	AY633472 Bacteriop
39	23	100.0	1241	7	AY633473 Bacteriop
40	23	100.0	1242	6	E30432 Method for
41	23	100.0	1254	1	AB015057 Escherich
42	23	100.0	1254	1	AB030484 Escherich
43	23	100.0	1254	6	AR433378 Sequence
44	23	100.0	1254	6	AX139386 Sequence
45	23	100.0	1254	6	BD010259 Nucleic a

ALIGNMENTS

RESULT 1	AX106740	Sequence 8 from Patent WO0123607.	23 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106740					
DEFINITION	AX106740					
ACCESSION	AX106740					
VERSION	AX106740.1	GI:13922401				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS	Gunzer, P. and Bellin, T.					
TITLE	Multiplex per for detecting ehac infections					
JOURNAL	Patent: WO 0123607-A 8 05-APR-2001;					
FEATURES	Roche Diagnostics GmbH (DE)					
SOURCE	location/Qualifiers					
	1..23					
	/organism="Escherichia coli"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:562"					
ORIGIN						
Query Match	100.0%;	Score 23;	DB 6;	Length 23;		
Best Local Similarity	100.0%;	Pred. No. 0.54;				
Matches	23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	AGCAGAAGCCTTACGCTTCAGGC	23			
Db	1	AGCAGAAGCCTTACGCTTCAGGC	23			
RESULT 2	AR099864	Sequence 5 from patent US 6080400.	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864					
DEFINITION	AR099864					
ACCESSION	AR099864					
VERSION	AR099864.1	GI:12810312				
KEYWORDS						
SOURCE						
ORGANISM						
	Unknown.					
	Unclassified.					

Best Local Similarity 100.0%; Pred. No. 0.011;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 177.005 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcgaagcctacgtccagc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	5	AA61485 EHEC pig
2	23	100.0	282	12	ADN02038 Enterohae
3	23	100.0	954	2	AA742651 Verotoxig
4	23	100.0	954	3	AA551196 E. coli v
5	23	100.0	954	6	ABK11777 E. coli v
6	23	100.0	980	2	AA742665 Histidine
7	23	100.0	981	3	AA551210 Recombina
8	23	100.0	981	6	ABK11791 Abk11791
9	23	100.0	989	3	AA742674 FLAG tag/
10	23	100.0	990	3	AA551219 FLAG tag-
11	23	100.0	990	6	ABK11800 CDNA enco
12	23	100.0	1201	2	AAV11405 Shiga tox
13	23	100.0	1217	2	AAV11406 Shiga tox
14	23	100.0	1232	11	ADL25585 E. cloacae
15	23	100.0	1232	11	ADL25580 E. coli s
16	23	100.0	1232	11	ADL25578 E. coli s
17	23	100.0	1234	11	ADL25581 E. coli s
18	23	100.0	1235	2	AA742654 Sequence
19	23	100.0	1235	3	AA551199 DNA direc
20	23	100.0	1235	6	ABK11780 Polyclon
21	23	100.0	1242	3	AA744676 E. coli s

22	23	100.0	1254	4	AA611779	AA611779 Escherich
23	23	100.0	1254	10	ADH22653	Adh22653 Escherich
24	23	100.0	1259	4	AAH01086	Aah01086 Escherich
25	23	100.0	1479	2	AAV11401	AAV11401 Shiga tox
26	23	100.0	1612	8	ACA64707	ACA64707 Verotoxin
27	23	100.0	1612	10	ADF43307	Adf43307 Superant
28	23	100.0	1664	2	AA227688	AA227688 Verotoxin
29	23	100.0	2085	3	AAA51227	AA51227 MBP-VT-2
30	23	100.0	2085	6	ABK11958	Abk11958 CDNA enco
31	23	100.0	2135	2	AA742672	AA742672 Maltoze b
32	23	100.0	2136	3	AA551217	AA551217 MBP-VT-2
33	23	100.0	2136	6	ABK11798	Abk11798 CDNA enco
34	23	100.0	61663	9	ACD19049	Accl19049 E. coli 0
35	23	100.0	62708	10	ADC00199	Adnc00199 Enterohae
36	23	100.0	134141	6	ABN83487	Abn83487 Escherich
37	23	93.0	960	10	ADH34345	Adh34345 Verotoxin
38	21.4	93.0	960	10	ADH34301	Adh34301 Verotoxin
39	21.4	93.0	960	10	ADH34343	Adh34343 Verotoxin
40	21.4	93.0	1234	11	ADL25582	Adl25582 E. coli s
41	21.4	93.0	1235	11	ADL25584	Adl25584 E. coli s
42	21.4	93.0	1235	11	ADL25583	Adl25583 E. coli s
43	19.8	86.1	960	10	ADH34339	Adh34339 Verotoxin
44	19.8	86.1	960	10	ADH34337	Adh34337 Verotoxin
45	18.4	80.0	576	10	ADD33754	Add33754 Mouse mlt

ALIGNMENTS

RESULT 1
ID AAF61485 standard; DNA; 23 BP.
AC AAF61485;
DT 18-JUN-2001 (first entry)
DE EHEC pig pathogen strx2 probe SEQ ID 8.
XX EHEC infection; multiplex amplification; detection; human; pig;
KW enterohemorrhagic Escherichia coli infection; pathogen; probe; ss.
XX Escherichia coli.
OS
PM DE19946296-Al.
PD 29-MAR-2001.
PF 28-SEP-1999; 99DE-01046296.
PR 28-SEP-1999; 99DE-01046296.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX Gunzer F, Bellin T;
PI WPI; 2001-246145/26.
DR
XX Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
PT in multiplex amplification detection of enterohemorrhagic strains.
XX
PS Claim 11; Page 11; 14pp; German.
XX This invention describes a novel primer (P1) which can be used in a
CC multiplex amplification reaction for detecting clinically important EHEC
CC (enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous
CC detection of human and pig pathogens in a single measurement
SQ Sequence 23 BP; 6 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 45.4639 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagcttcgcttgcactgtca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	954	3	US-08-816-977-5
2	28	100.0	954	4	US-09-334-477-5
3	28	100.0	981	3	US-08-816-977-24
4	28	100.0	981	4	US-09-334-477-24
5	28	100.0	990	3	US-08-816-977-38
6	28	100.0	990	4	US-09-334-477-38
7	28	100.0	1235	3	US-08-816-977-10
8	28	100.0	1235	4	US-09-334-477-10
9	28	100.0	1254	4	US-09-599-032A-3
10	28	100.0	2085	3	US-08-816-977-48
11	28	100.0	2085	4	US-09-334-477-48
12	28	100.0	2136	3	US-08-816-977-34
13	28	100.0	2136	4	US-09-334-477-34
14	28	100.0	61663	3	US-09-453-702B-62
15	19.6	70.0	1038	4	US-09-248-796A-11678
16	18.2	65.0	2406	4	US-09-543-681A-3389
17	17.8	63.6	327	4	US-09-248-796A-11059
18	17.8	63.6	527	4	US-09-621-976-16905
19	17.4	62.1	582	4	US-09-976-594-516
20	17.4	62.1	2483	2	US-08-177-109A-1
21	17.4	62.1	2483	2	US-08-687-706-1
22	17.4	62.1	2505	4	US-09-799-451-179
23	17.4	62.1	2733	4	US-09-976-594-517
24	17.2	61.4	74	4	US-09-508-930D-45
25	17.2	61.4	810	4	US-09-543-681A-2228
26	17	60.7	846	3	US-09-134-001C-1012
27	17	60.7	1767	4	US-09-601-198-72

28	17	60.7	4832	4	US-08-956-171E-189	Sequence 189, App
29	17	60.7	4832	4	US-08-781-986A-189	Sequence 189, App
30	17	60.7	7070	1	US-08-619-554-3	Sequence 3, Appl1
31	17	60.7	12685	4	US-09-479-467A-3	Sequence 3, Appl1
32	16.8	60.0	168	2	US-08-447-173A-53	Sequence 53, Appl
33	16.8	60.0	235	4	US-09-513-999C-26560	Sequence 26560, A
34	16.8	60.0	238	4	US-09-270-767-7511	Sequence 7511, Ap
35	16.8	60.0	238	4	US-09-270-767-22793	Sequence 22793, A
36	16.8	60.0	420	4	US-09-513-999C-28267	Sequence 28267, A
37	16.8	60.0	558	4	US-09-248-796A-10214	Sequence 10214, A
38	16.8	60.0	670	3	US-09-306-446C-15	Sequence 15, Appl
39	16.8	60.0	779	1	US-08-592-214A-9	Sequence 9, Appl1
40	16.8	60.0	779	3	US-08-659-188-9	Sequence 9, Appl1
41	16.8	60.0	779	3	US-08-655-227-9	Sequence 9, Appl1
42	16.8	60.0	779	3	US-08-655-241-9	Sequence 9, Appl1
43	16.8	60.0	779	3	US-09-149-976-9	Sequence 9, Appl1
44	16.8	60.0	779	3	US-09-398-326-9	Sequence 9, Appl1
45	16.8	60.0	1541	4	US-09-518-914-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Veroxoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
MOLCULE TYPE: DNA (genomic)
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 28; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 / Search time 1927.24 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 1 agagcagcttcgcttcgttcacactgca 28

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est8:*

9: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	73.6	635	BZ887470	CH240_198
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3	20.6	73.6	806	BZ159158	CH230-376
4	20.6	73.6	897	CB197911	AGENCOURT
5	20.6	73.6	962	CC735187	OGVBE92TH
6	20.6	73.6	1468	CN905340	Retradon
7	20.2	72.1	858	A1422096	tf57h05.x
8	20.2	71.4	527	BZ342868	AL837591
9	20.2	71.4	529	CC578661	CH240_457
10	20.2	71.4	825	BI737664	603358577
11	20.2	71.4	822	BI550495	603195417
12	20.2	71.4	893	BU132590	60312189
13	20.2	71.4	893	BU132590	60312189
14	20.2	71.4	1225	BG115160	603316031
15	19.8	70.7	631	BU221953	603754843
16	19.8	70.7	729	BU258365	603742872
17	19.8	70.7	1144	CL052971	CH216-76N
18	19.8	70.7	478	AG431086	HS_5087.7
19	19.6	70.0	605	CF112629	Shltzom1
20	19.6	70.0	627	AG421708	1M020005
21	19.6	70.0	726	AG0840728	nbxb0068L
22	19.6	70.0	779	BH073448	RPCI-24-2
23	19.6	70.0	802	CF289530	AGENCOURT
24	19.6	70.0	802	CF289530	AGENCOURT

C 25	19.6	70.0	1147	2	BF039006	BF039006
C 26	19.4	69.3	372	7	CO219380	CO219380
C 27	19.4	69.3	372	7	CO219380	CO219380
C 28	19.2	68.6	226	9	CE657761	CE657761
C 29	19.2	68.6	375	5	BI447986	BI447986
C 30	19.2	68.6	467	9	CE659430	CE659430
C 31	19.2	68.6	487	9	CE659430	CE659430
C 32	19.2	68.6	503	9	CE659430	CE659430
C 33	19.2	68.6	522	9	CE447512	CE447512
C 34	19.2	68.6	574	9	CE332237	CE332237
C 35	19.2	68.6	584	9	CE644007	CE644007
C 36	19.2	68.6	618	9	CE274455	CE274455
C 37	19.2	68.6	628	9	CE573420	CE573420
C 38	19.2	68.6	686	1	AU005087	AU005087
C 39	19.2	68.6	703	9	CE133005	CE133005
C 40	19.2	68.6	707	9	BQ898634	BQ898634
C 41	19.2	68.6	957	5	CL034070	CL034070
C 42	19.2	68.6	1023	9	AM892893	AM892893
C 43	19.2	67.9	289	8	BZ155702	BZ155702
C 44	19.2	67.9	350	8	BZ155702	BZ155702
C 45	19.2	67.9	403	7	T95154	T95154

ALIGNMENTS

RESULT 1
BZ887470
LOCUS
DEFINITION
CH240_198C16.TV CHORI-240 Bos taurus genomic clone CH240_198C16,
genomic survey sequence.

ACCESSION
BZ887470
VERSION
BZ887470.1 GI:29114872
KEYWORDS
GSS.

SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus

REFERENCE
Zhao S., Shetty J., Shatsman S., Tsagaye G., Geer K.,
Shvartsbeyn A., Gebregorgis E., Chen D., Riggs F., de Jong P.,
Crawford A.M. and McMan J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdjong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by AgResearch Ltd., New Zealand and The
Institute of Genomic Research (TIGR), USA.

Plate: 198 row: C column: 16
Seg primer: SP6
Class: BAC ends.

Location/Qualifiers
1..635

FEATURES
source
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_198C16"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 : Search time 1593.09 Seconds

(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23
Sequence: 1 agcgaagcctcagctcagc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.8	86.1	632	2	BB608995 BB608995
C 2	19.8	86.1	2148	3	AK054278 Mus muscu
C 3	19.4	84.3	590	5	BQ121748 EST607324
C 4	19.4	84.3	596	4	BG592107 EST499949
C 5	19.4	84.3	597	5	BQ121747 EST607323
C 6	18.8	81.7	303	5	BY032941 BY032941
C 7	18.4	80.0	346	9	CG69077 AB0259 Sa
C 8	18.4	80.0	356	5	BY136877 BY136877
C 9	18.4	80.0	361	5	BY133551 BY133551
C 10	18.4	80.0	380	5	CC200394 RRB094 Ba
C 11	18.4	80.0	381	9	CG561824 OST183711
C 12	18.4	80.0	392	1	AI930332 u163d05.Y
C 13	18.4	80.0	400	5	CG607518 OST286486
C 14	18.4	80.0	419	5	BY035663 BY035663
C 15	18.4	80.0	422	5	BY227863 BY227863
C 16	18.4	80.0	424	5	CG523885 OST196839
C 17	18.4	80.0	427	7	W83819 mE33903.r1
C 18	18.4	80.0	437	5	BY252038 BY252038
C 19	18.4	80.0	447	9	CG574608 OST207631
C 20	18.4	80.0	452	2	BB137544 u664901.Y
C 21	18.4	80.0	454	9	CG610742 OST194781
C 22	18.4	80.0	468	6	CP160973 B0691H11-
C 23	18.4	80.0	474	4	BG971552 602838094

C 25	18.4	80.0	479	1	AI116569 ud74h06.Y
C 26	18.4	80.0	483	4	BG061488 B0130B09-
C 27	18.4	80.0	494	6	CA886486 B0130B09-
C 28	18.4	80.0	498	1	AA914041 vY97c01.r
C 29	18.4	80.0	501	5	BX521078 BX521078
C 30	18.4	80.0	505	9	CG654782 CG654782
C 31	18.4	80.0	508	6	CA884326 B0109D12-
C 32	18.4	80.0	512	7	CG683644 B0109D12-
C 33	18.4	80.0	513	7	CG604615 A0934D09-
C 34	18.4	80.0	517	9	CG604615 A0934D09-
C 35	18.4	80.0	520	1	AI255684 AI255684
C 36	18.4	80.0	522	1	AI156947 AI156947
C 37	18.4	80.0	523	6	CP166500 CP166500
C 38	18.4	80.0	529	2	BE370517 BE370517
C 39	18.4	80.0	533	2	AM611168 AM611168
C 40	18.4	80.0	537	2	AM012317 AM012317
C 41	18.4	80.0	546	2	BE134721 BE134721
C 42	18.4	80.0	548	6	CA551676 CA551676
C 43	18.4	80.0	549	2	AM012224 AM012224
C 44	18.4	80.0	551	2	BF100103 BF100103
C 45	18.4	80.0	570	2	AM412918 uq50g03.Y

ALIGNMENTS

RESULT 1
LOCUS BB608995/c 632 bp mRNA linear EST 26-OCT-2001
DEFINITION BB608995 RIKEN full-length enriched, 2 days pregnant adult female
ovary Mus musculus cDNA clone E33009J08 5', mRNA sequence.

ACCESSION BB608995
VERSION BB608995.2 GI:16451136
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 632)
Araaka,T., Carninci,P., Fukuda,S., Furuno,M., Hangaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Konda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Takeda,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Araaka,T., et al. 2001)
Unpublished (2001)
On Dec 6, 2000 this sequence version replaced gi:11564171.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

TITLE

JOURNAL

COMMENT

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waghi,K., Fujiwara,S., Inoue,K., Togawa,Y., Itawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 : Search time 1651.92 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24
Sequence: 1.tgccacagctgcgtcagtgagct 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	164	4	EG384763
2	19.8	82.5	864	8	BZ137613
3	19.2	80.0	319	6	BY794428
4	19.2	80.0	331	5	BY145728
5	19.2	80.0	366	5	BY168177
6	19.2	80.0	380	2	BB842411
7	19.2	80.0	462	2	BB842411
8	19.2	80.0	483	6	CB545045
9	19.2	80.0	573	9	AO570333
10	19.2	80.0	697	9	CR022070
11	19.2	80.0	717	2	BS569949
12	19.2	80.0	865	4	CB131571
13	19.2	80.0	866	4	BI659266
14	19.2	80.0	1262	6	CA492803
15	19.2	80.0	3022	3	AK004595
16	19.2	80.0	3124	3	BC027329
17	19.2	80.0	3214	3	BC048910
18	18.8	78.3	711	9	AG335488
19	18.8	78.3	749	9	AG442797
20	18.8	78.3	753	9	CE321712
21	18.2	75.8	385	6	BY647886
22	18.2	75.8	424	8	AO681986
23	18.2	75.8	450	1	AU062893
24	18.2	75.8	480	2	BF603001

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
25	18.2	75.8	520	7	AK2107635									
26	18.2	75.8	563	8	AQ122468									
27	18.2	75.8	624	8	AZ759334									
28	18.2	75.8	680	8	BZ737939									
29	18.2	75.8	758	9	CC726778									
30	18.2	75.8	765	9	CC708643									
31	18.2	75.8	789	9	BZ737943									
32	18.2	75.8	791	6	CD47854									
33	18.2	75.8	856	9	CNS05851									
34	18.2	75.8	857	5	B0205885									
35	18.2	75.8	1011	9	CG348401									
36	18.2	75.8	1020	9	CL209120									
37	18.2	75.8	1020	9	CG348401									
38	17.8	74.2	190	4	EG305521									
39	17.8	74.2	191	8	AZ251801									
40	17.8	74.2	260	7	CN168920									
41	17.8	74.2	373	2	AW154327									
42	17.8	74.2	437	6	CA951575									
43	17.8	74.2	495	8	AZ878920									
44	17.8	74.2	512	8	AQ933350									
45	17.8	74.2	522	7	CK383349									

ALIGNMENTS

RESULT 1
EG384763
LOCUS EG384763 164 bp mRNA linear EST 12-MAR-2001
DEFINITION 304043 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION EG384763
VERSION EG384763.1 GI:13309235
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
1 (bases 1 to 164)
Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Perce, G., Sultana, R.,
Quackenbush, J., and Keefe, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
JOURNAL MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR PRIMERs
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 92 row: P column: 18
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 164
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/feature_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 1P1G"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

FEATURES
SOURCE
ORIGIN

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OW nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1445.43 Seconds

(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21
Sequence: 1 cgatactccgaagacacattg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	87.6	481	9	CC880516 ZM880516
C 2	18.4	87.6	799	9	CC830906 ZM880516
C 3	17.8	84.8	302	5	BQ37313 RC5-FT019
C 4	17.4	82.9	740	9	CL196951 104_423_1
C 5	17.4	82.9	844	2	BF796995 602258028
C 6	17	81.0	443	2	AM872041 da96d01.y
C 7	17	81.0	543	4	Bu613139 Bu613139
C 8	17	81.0	554	4	B1442079 B1442079
C 9	17	81.0	689	5	CB593139 AGENCOURT
C 10	17	81.0	720	5	BP726595 BP726595
C 11	17	81.0	758	5	BP723599 BP723599
C 12	17	81.0	760	7	BP688365 BP688365
C 13	17	81.0	762	7	BP692248 BP692248
C 14	17	81.0	809	6	CA789606 AGENCOURT
C 15	17	81.0	812	6	CD360247 CD360247
C 16	17	81.0	826	6	CD301144 AGENCOURT
C 17	17	81.0	852	6	CD361666 AGENCOURT
C 18	17	81.0	852	6	CD361666 AGENCOURT
C 19	17	81.0	877	6	CB196834 AGENCOURT
C 20	17	81.0	927	6	CD302134 AGENCOURT
C 21	16.8	80.0	933	6	CA973359 AGENCOURT
C 22	16.8	80.0	371	7	CF501009 MS1-0038U
C 23	16.8	80.0	380	6	CD186770 MS1-0056U
C 24	16.8	80.0	391	9	CG416831 ZM880516

25	16.8	80.0	393	9	CG416853
26	16.8	80.0	438	9	AG194060
27	16.8	80.0	442	2	BP858265
28	16.8	80.0	453	1	AV736811
C 29	16.8	80.0	472	6	CD163413
C 30	16.8	80.0	477	7	CF503348
C 31	16.8	80.0	481	8	AO570770
C 32	16.8	80.0	550	8	BH203322
C 33	16.8	80.0	559	8	BH203322
C 34	16.8	80.0	668	9	CG868976
C 35	16.8	80.0	690	7	CF500020
C 36	16.8	80.0	694	8	CC175967
C 37	16.8	80.0	695	3	AY432489
C 38	16.8	80.0	723	7	CN038101
C 39	16.8	80.0	729	2	BF793256
C 40	16.8	80.0	777	9	CG200402
C 41	16.8	80.0	778	9	CG703102
C 42	16.8	80.0	815	2	BE793728
C 43	16.8	80.0	918	4	BG388642
C 44	16.8	80.0	1037	9	CG423348
C 45	16.8	80.0	1044	9	CG685298

ALIGNMENTS

RESULT 1
LOCUS CC880516/c 481 bp DNA linear GSS 29-JUL-2003
DEFINITION ZM880516A02.f ZM880516 Zea mays genomic clone ZM880516A02 5',
ACCESSION CC880516
VERSION CC880516.1 GI:33315097
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 481)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wang, R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0218 row: A column: 02
Seq primer: T7
Class: BAC ends.

FEATURES

source
location/Qualifiers

1..481
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="B73"
/db_xref="taxon:4577"
/clone="ZM880516A02"
/lab_host="DH10B"
/clone_lib="ZM880516"
/note="Vector: pBeloBAC11, Site 1: HindIII, Site 2:
HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 481;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1651.92 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-2
Perfect score: 24
Sequence: 1 ccggacacatagaagaactcat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.8	86.7	949	3	CR670603 Tetraodon
2	19.8	82.5	680	7	CN326151 AGENCOURT
3	19.2	80.0	156	2	AW885334 QV4-OT006
4	19.2	80.0	763	9	CNS049GR
5	19.2	80.0	805	9	CE323459
6	19.2	80.0	940	9	CNS04H7J
7	18.8	78.3	483	4	BI138333
8	18.8	78.3	528	4	CKO91504
9	18.8	78.3	530	7	CKI01628
10	18.4	76.7	618	5	BP724915
11	18.4	76.7	452	7	BH320282
12	18.4	76.7	579	8	BH320282
13	18.4	76.7	914	8	BH320282
14	18.2	75.8	101	8	BZ236055
15	18.2	75.8	114	7	CR434085
16	18.2	75.8	308	1	AL962135
17	18.2	75.8	311	1	AL955012
18	18.2	75.8	347	5	BP675436
19	18.2	75.8	360	1	AU245212
20	18.2	75.8	360	1	AU245212
21	18.2	75.8	375	1	AU245214
22	18.2	75.8	381	4	AU244659
23	18.2	75.8	387	7	CF786403
24	18.2	75.8	392	1	AL644866

C 25	18.2	75.8	401	1	AL875276	AL875276
C 26	18.2	75.8	406	8	CC057478	CC057478
C 27	18.2	75.8	408	7	CN109513	CN109513
C 28	18.2	75.8	409	1	AL787946	AL787946
C 29	18.2	75.8	414	1	AL794318	AL794318
C 30	18.2	75.8	429	7	CN119667	CN119667
C 31	18.2	75.8	436	1	AL774003	AL774003
C 32	18.2	75.8	445	1	AL968405	AL968405
C 33	18.2	75.8	456	7	CN119519	CN119519
C 34	18.2	75.8	458	7	CN114585	CN114585
C 35	18.2	75.8	467	1	AL970785	AL970785
C 36	18.2	75.8	477	1	AL791399	AL791399
C 37	18.2	75.8	482	1	AL777926	AL777926
C 38	18.2	75.8	484	4	BU611732	BU611732
C 39	18.2	75.8	486	2	AL791571	AL791571
C 40	18.2	75.8	492	2	AW147738	AW147738
C 41	18.2	75.8	507	4	BG553712	BG553712
C 42	18.2	75.8	510	7	CN119608	CN119608
C 43	18.2	75.8	512	4	BU633081	BU633081
C 44	18.2	75.8	513	1	AL673077	AL673077
C 45	18.2	75.8	513	4	BG162432	BG162432

ALIGNMENTS

RESULT 1
LOCUS CR670603/c 949 bp mRNA linear HTC 11-AUG-2004
DEFINITION Tetraodon nigroviridis full-length cDNA.
ACCESSION CR670603
VERSION CR670603.1 GI:51167048
KEYWORDS HTC, cDNA, full-length, Tetraodon nigroviridis.
SOURCE Tetraodon
ORGANISM Tetraodon
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae.
1 (bases 1 to 949)
Genoscope.
Direct Submission
Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
(E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

FEATURES

source location/Qualifiers
1..949
/organism="Tetraodon"
/mol_type="mRNA"
/db_xref="taxon:47144"
/cissue_type="muscle"

ORIGIN

Query Match 86.7%; Score 20.8; DB 3; Length 949;
Best Local Similarity 91.7%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 CCGGACATATGAAAGAACTCAT 24
24 CCGGACATATGAAAGAACTCAT 1

RESULT 2
LOCUS CN326151 680 bp mRNA linear EST 14-APR-2004
DEFINITION AGENCOURT 22000357 NICHD XGC Te2 Xenopus laevis cDNA clone
IMAGE:7207027 3', mRNA sequence.
ACCESSION CN326151
VERSION CN326151.1 GI:46383787
KEYWORDS EST.

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52, Search time 38.9691 seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-2
Perfect score: 24
Sequence: 1 ccgacacacatagaagaactcat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	945 3 US-08-816-977-1	Sequence 1, Appl
2	24	100.0	945 4 US-09-334-477-1	Sequence 1, Appl
3	24	100.0	969 3 US-08-816-977-20	Sequence 20, Appl
4	24	100.0	969 4 US-09-334-477-20	Sequence 20, Appl
5	24	100.0	981 3 US-08-816-977-36	Sequence 36, Appl
6	24	100.0	981 4 US-09-334-477-36	Sequence 36, Appl
7	24	100.0	1241 3 US-08-816-977-9	Sequence 9, Appl
8	24	100.0	1241 4 US-09-334-477-9	Sequence 9, Appl
9	24	100.0	2073 3 US-08-816-977-46	Sequence 46, Appl
10	24	100.0	2073 4 US-09-334-477-46	Sequence 46, Appl
11	24	100.0	2127 3 US-08-816-977-32	Sequence 32, Appl
12	24	100.0	2127 4 US-09-334-477-32	Sequence 32, Appl
13	24	100.0	48908 3 US-09-453-7028-137	Sequence 137, App
14	19	79.2	70 1 US-07-988-430-75	Sequence 75, Appl
15	19	79.2	70 1 US-08-425-336-73	Sequence 73, Appl
16	19	79.2	70 1 US-08-488-113B-73	Sequence 73, Appl
17	19	79.2	70 1 US-08-477-484B-73	Sequence 73, Appl
18	19	79.2	70 2 US-08-646-360-73	Sequence 73, Appl
19	19	79.2	70 3 US-08-839-765-73	Sequence 73, Appl
20	19	79.2	70 3 US-09-136-389-73	Sequence 73, Appl
21	19	79.2	70 3 US-09-610-838-73	Sequence 73, Appl
22	19	79.2	70 4 US-09-711-485-73	Sequence 73, Appl
23	19	79.2	70 5 PCT-US92-09487-75	Sequence 75, Appl
24	19	79.2	78 1 US-07-988-430-76	Sequence 76, Appl
25	19	79.2	78 1 US-08-425-336-74	Sequence 74, Appl
26	19	79.2	78 1 US-08-488-113B-74	Sequence 74, Appl
27	19	79.2	78 1 US-08-477-484B-74	Sequence 74, Appl

28	19	79.2	78 2 US-08-646-360-74	Sequence 74, Appl
29	19	79.2	78 3 US-08-839-765-74	Sequence 74, Appl
30	19	79.2	78 3 US-09-136-389-74	Sequence 74, Appl
31	19	79.2	78 3 US-09-610-838-74	Sequence 74, Appl
32	19	79.2	78 4 US-09-711-485-74	Sequence 74, Appl
33	19	79.2	78 5 PCT-US92-09487-76	Sequence 76, Appl
34	19	79.2	78 5 PCT-US92-09487-76	Sequence 76, Appl
35	19	79.2	1072 2 US-08-621-803-250	Sequence 250, App
36	17.2	71.7	2484 4 US-09-217-352-250	Sequence 250, App
37	16.8	70.0	513 4 US-09-621-976-3864	Sequence 68, Appl
38	16.6	69.2	903 4 US-09-534-228B-6	Sequence 1864, Ap
39	16.6	69.2	2151 4 US-09-134-000C-230	Sequence 230, App
40	16.6	69.2	1664976 4 US-08-916-642B-1	Sequence 11481, A
41	16.6	69.2	1664976 4 US-08-916-642B-1	Sequence 1, Appl
42	16.6	69.2	1664976 4 US-08-916-642B-1	Sequence 1, Appl
43	16.4	68.3	32768 4 US-09-692-570-1	Sequence 71, Appl
44	16.2	67.5	363 4 US-09-513-999C-17385	Sequence 17385, A
45	16.2	67.5	441 4 US-09-621-976-9317	Sequence 9317, Ap

ALIGNMENTS

RESULT 1
US-08-816-977-1/c
Sequence 1, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPMD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8538
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURES:
NAME/KEY: CDS
LOCATION: 1..945
US-08-816-977-1
Query Match 100.0%; Score 24; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1376.6 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-3

Perfect score: 20

Sequence: 1 ttccggaatgcacatcagtc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gest1:*

9: gb_gest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	87.0	181	1	AV112270 AV112270
C 2	17.4	87.0	229	1	AV361260 AV361260
C 3	17.4	87.0	675	8	BH9882496 BH9882496
C 4	17.4	87.0	910	6	CA472629 AGNCCOURT
C 5	16.8	84.0	203	9	CE577268 tigr-g88
C 6	16.8	84.0	229	7	CO371015 tcn86d04
C 7	16.8	84.0	234	2	BH166371 BH166371
C 8	16.8	84.0	253	2	BH221661 BH221661
C 9	16.8	84.0	292	5	B0626804 pz27c05.y
C 10	16.8	84.0	340	7	CO746789 tcn94f12
C 11	16.8	84.0	417	5	BU429239 UT-HF-BNO
C 12	16.8	84.0	456	5	BQ482167 ke50f05.y
C 13	16.8	84.0	480	5	AM547090 L0017B07
C 14	16.8	84.0	485	5	BQ482333 ke56a02.y
C 15	16.8	84.0	485	5	BQ482335 ke56a02.y
C 16	16.8	84.0	490	5	BQ482330 ke58d01.y
C 17	16.8	84.0	502	5	BQ482357 ke58d07.y
C 18	16.8	84.0	513	5	BQ482145 ke50b10.y
C 19	16.8	84.0	579	7	CN775343 tae72c04
C 20	16.8	84.0	586	7	CO371014 tcn86d03
C 21	16.8	84.0	597	7	CO371002 tcn86d08
C 22	16.8	84.0	621	5	BX505754 DKFZP6860
C 23	16.8	84.0	653	8	AZ358338 IM0100A18
C 24	16.8	84.0			

C 25	16.8	84.0	663	9	CE507740 tigr-g88
C 26	16.8	84.0	759	9	AG478858 Mus muscu
C 27	16.8	84.0	785	2	BF862749 BF862749
C 28	16.8	84.0	829	9	BG698414 BG698414
C 29	16.8	84.0	902	9	CC549036 CH240.433
C 30	16.8	84.0	261	4	BI241119 RB38135.5
C 31	16.4	82.0	282	4	BI355815 CM32465.5
C 32	16.4	82.0	294	4	BI243027 RB4056.5
C 33	16.4	82.0	385	1	AI617042 zehno094
C 34	16.4	82.0	403	1	AA695947 GM04817.5
C 35	16.4	82.0	414	2	AW771236 hm61b02.x
C 36	16.4	82.0	423	4	BI883805 tno7e01.y
C 37	16.4	82.0	489	1	AA695937 GM04803.5
C 38	16.4	82.0	489	4	BI430369 tgn0c06.y
C 39	16.4	82.0	551	2	BE557055 t109f10.y
C 40	16.4	82.0	552	5	BO285434 faa30a12
C 41	16.4	82.0	574	4	BG892067 fg90c06.y
C 42	16.4	82.0	578	4	BI229069 RE26772.5
C 43	16.4	82.0	600	5	BU925349 7121-15 M
C 44	16.4	82.0	609	4	BI242268 RB39556.5
C 45	16.4	82.0	631	5	BQ449484 faa47g11

ALIGNMENTS

RESULT 1
AV112270/c 181 bp mRNA linear EST 29-JUN-1999
LOCUS AV112270 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
DEFINITION clone 2610010N22, mRNA sequence.
VERSION AV112270
ACCESSION AV112270.1 GI:5266350
KEYWORDS
SOURCE
ORGANISM
MUS musculus (house mouse)
REFERENCE
AUTHORS
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Mitsuuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagami, K., Yamamura, T., Yokote, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098

TITLE
JOURNAL
COMMENT

Email: genome-res@tc.riken.go.jp
Thermolabile and thermostable DNA polymerase by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.ttc.riken.go.jp) for
further details.

FEATURES
source

1. 181
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/clone="2610010N22"
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 170.706 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21

Sequence: 1 cgatactccggaacacatg 21

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:
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2: /cgn2_6/prodata/2/pubpna/PCR_NEW_PUB.seq:*
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5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/PCRUS_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	100.0	954	9	US-09-334-477-5	Sequence 5, Appl1
C 2	100.0	981	9	US-09-334-477-24	Sequence 24, Appl1
C 3	100.0	990	9	US-09-334-477-38	Sequence 38, Appl1
C 4	100.0	1235	9	US-09-334-477-10	Sequence 10, Appl1
C 5	100.0	1612	9	US-09-870-759-27	Sequence 27, Appl1
C 6	100.0	1612	10	US-09-751-708A-27	Sequence 27, Appl1
C 7	100.0	1612	10	US-10-428-817A-23	Sequence 23, Appl1
C 8	100.0	1612	18	US-10-425-821-92	Sequence 92, Appl1
C 9	100.0	2085	9	US-09-334-477-48	Sequence 48, Appl1
C 10	100.0	2136	9	US-09-334-477-34	Sequence 34, Appl1
C 11	100.0	61662	16	US-10-418-837-1	Sequence 1, Appl1
C 12	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl1

Result No.	Score	Query Match	Length	ID	Description
C 13	16.8	80.0	2624	18	US-10-425-115-78451
C 14	16.8	80.0	5085	17	US-10-437-963-2350
C 15	16.8	80.0	6018	17	US-10-437-963-69454
C 16	16.4	78.1	562	16	US-10-424-599-41130
C 17	16.4	78.1	3411	17	US-10-437-963-78544
C 18	16.4	78.1	160142	13	US-10-027-633-55064
C 19	16.4	78.1	1601042	15	US-10-027-633-55064
C 20	16.4	76.2	4592	14	US-10-193-692-1
C 21	15.8	75.2	223	16	US-10-621-901-85
C 22	15.8	75.2	244	16	US-10-621-901-1858
C 23	15.8	75.2	478	17	US-10-767-701-20241
C 24	15.8	75.2	487	10	US-09-918-995-14811
C 25	15.8	75.2	1272	17	US-10-425-115-162587
C 26	15.8	75.2	1272	17	US-10-437-963-23246
C 27	15.8	75.2	1766	16	US-10-412-6998-205
C 28	15.8	75.2	1775	14	US-10-286-264-105
C 29	15.8	75.2	1783	16	US-10-425-114-12995
C 30	15.8	75.2	2046	9	US-09-764-898-95
C 31	15.8	75.2	2492	9	US-09-764-898-95
C 32	15.8	75.2	2971	18	US-10-425-115-22045
C 33	15.8	75.2	4672	13	US-10-194-163-846
C 34	15.8	75.2	4733	17	US-10-437-963-117
C 35	15.8	75.2	4736	9	US-09-822-830A-35
C 36	15.8	75.2	58965	15	US-10-298-122-2
C 37	15.8	75.2	149480	10	US-09-873-367C-284
C 38	15.8	75.2	149480	10	US-09-873-367C-285
C 39	15.8	75.2	149480	11	US-09-868-007A-232
C 40	15.4	73.3	366	8	US-08-781-986A-4332
C 41	15.4	73.3	366	16	US-10-329-624-4332
C 42	15.4	73.3	582	17	US-10-437-963-64485
C 43	15.4	73.3	732	16	US-10-424-599-73706
C 44	15.4	73.3	732	13	US-10-052-586-577
C 45	15.4	73.3	732	14	US-10-174-590-577

ALIGNMENTS

RESULT 1
US-09-334-477-5/C
; Sequence 5, Application US/09334477
; Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:

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